Tue May 11 11:56:46 2004

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{without alignments)
2194.362 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries
                                                      - nucleic search, using sw model
                                                                                                                                                                                                 IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                     Sequence:
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                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 90. Appl	Sequence 89, Appl	Sequence 7485, Ap	Sequence 1, Appli	Sequence 4833, Ap	Sequence 1, Appli	Sequence 188, App	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 649, App	Sequence 190, App	Sequence 2344, Ap	Sequence 3, Appli
SOUTHWINDS	Query Score Match Length DB ID	13249	43.2 42.8 13249 15 US-10-311-455-89	28.8 28.5 1989 15 US-10-156-761-7485	8.8 28.5 9025608 15 US-10-156-761-1	28.6 28.3 1596 15 US-10-156-761-4833	28.3 9025608 3	. 28.1 381 9	28.2 27.9 884 9 US-09-790-045-11	27.9 884 15	27.9 884 15	27.5 412 9	27.5 1735 16	27.5 2323 16	7.8 27.5 2483 14 US-10-143-002-3
	Result No. Sco		2 43	3 26	4 26	c 5 26	c 6 26	7 26	G 8 2E	c 9 26	G 10 2E	11 27	c 12 27	13 27	14 27
	EK.														

⊢ 10	Sequence 5868, Ap Sequence 5868, Ap Sequence 5868, Ap Sequence 341, App Sequence 39, Appl Sequence 39, Appl	7385 2381 101(511,		150, 144, 144, 1358, 50, 50,
p p	US-10-040-862-5868 US-10-057-475B-5868 US-10-154-884B-5868 US-09-764-853-341 US-09-764-881-39 US-09-764-881-39 US-10-242-747-39		US-1 US-1 US-1 US-0 US-1	ÞÞ
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27.5	226.327.1 26.327.1 26.39	26.9 26.9 26.9 26.9	26.7 26.7 26.7 26.7 26.7 26.7	26.7 26.7 26.7 26.7 26.7 26.7 26.7 26.7
227.8 27.7.8 27.7.6	4 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	22.72 22.72	22 22 22 72 72 72	04444444444444444444444444444444444444
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ALIGNMENTS

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Sequence 90, Application US/10311455
Fublication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
SEQ ID NOS: 2424
LENGTH: 13249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%; Score 55; DB 15; 78.8%; Pred. No. 1.3e-08; tive 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 78.8
Matches 78; Conservative
US-10-311-455-90/c
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                                                                                                          0
                                                     Length 1989;
                                                                                                          Indels
                                                  Score 28.8; DB 15;
Pred. No. 4.8;
0; Mismatches 37;
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LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, HARUOH
APPLICANT: SHIRA, HAROSHI
APPLICANT: SHIRA, TADAXOSHI
APPLICANT: SHIRA, TADAXOSHI
APPLICANT: SHIRA, TADAXOSHI
APPLICANT: HATTORI MASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFERENCE: 249-226
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
RIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
SRIOR PILING DATE: 2001-06-30
FRIOR PILING DATE: 2001-06-30
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SHIRA, TADAVOSHI
APPLICANT: SAKAKI, VOSHIVUKI
APPLICANT: ARAPORI, MASAHIRA
IITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                       504 CATCCCGTACGAGGCCCATGACCCGGGC 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10156761
Publication No. US20030119018A1
                                                  28.5%;
                                                  Query Match
Best Local Similarity 58.0°
Matches 51; Conservative
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US-10-156-761-7485
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Sequence 89, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: SEMIN' Kurt

TITLE OF INVENTION: Cytosine methylation
ITILE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-89
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9030 ACACCCTTCCAAACATTTACCCGCCGCGATTCAAAAAC 8992
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APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERRNCE: 249-262
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PLLING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PLLING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7485
LENGTH: 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(1989)
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US-10-156-761-7485
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NAME/KEY: CDS
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APPLICANT: Hasebe, Akira
APPLICANT: Tsuchiya, Kenichi
APPLICANT: Horita, Mitsuo
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia Solanacearum
FILE REFERENCE: NANP108US
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                                  Sequence 188 Application US/09925297

Sequence 188 Application US/09925297

Patent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: ROSE et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: FCT/US00/05989

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 188
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53.7%; Pred. No. 7.3;
Live 6; Mismatches 32;
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CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
LENGTH: 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: (293)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (350)
; OTHER INFORMATION: n equals a,t,g, or
US-09-925-297-188
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; Patent No. US20020052047A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Ralstonia solanacearum FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
27.9%;
Best Local Similarity 59.3%;
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY: CDS
, LOCATION: (44)...(865)
US-09-790-045-11
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Best Local Similarity
Matches 44; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-790-045-11/c
                               US-09-925-297-188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ACCTGGGGGTCAGGCCCCCAGGGAAGCGCGCCCAAGGAGCGCGCGAAACCTTCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.6; DB 15; Length 9025608; Pred. No. 3.2; 0; Mismatches 39; Indels 0; G
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                                                                                                                                                                                                                                                                                                                                                                             Length 1596;
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                                                                                                                                                                                                                                                                                                                                                                                                                             39;
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LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
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Pred. No. 5.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CACCCTTCCAGGCATTTGCCCGCCGCGATTC 94
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIXAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATYORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO :
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: UP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-06-30
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4833
; LENGTH: 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local Similarity 57.1%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                ) NAME/KEY: CDS
; LOCATION: (1)..(1596)
US-10-156-761-4833
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TYPE: DNA
CONGANISM: Homo sapiens
US-09-833-381-649
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APPLICANT: Hasebe, Akira
APPLICANT: Tsuchiya, Kenichi
APPLICANT: Tsuchiya, Kenichi
APPLICANT: Horita, Mitsuo
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia
TITLE OF INVENTION: Solanacearum
FILE REFERENCE: NAMPIO8US
CURRENT APPLICATION NUMBER: US/10/222,577
CURRENT FILING DATE: 2002-08-16
PRIOR FILING DATE: 2001-02-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 GGGGTCAGGCCCCAGCCGCGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCCCACACCC
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                            195 crcakérégcacrécédadéd 175
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                                                                                                     Sequence 11, Application US/10222577 Publication No. US20030009026A1 GENERAL INFORMATION:
89
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ORGANISM: Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Ralstonia solanacearum
69 TTCCAGGCATTTGCCCGCCGC
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; LOCATION: (44)...(865)
US-10-222-578-11
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; LOCATION: (44)...(865)
US-10-222-577-11
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Matches 48; Conserv
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US-10-222-578-11/c
                                                                                              US-10-222-577-11/c
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US-09-833-381-649
Squence 649, Application US/09833381
Squence 649, Application US/09833381
GENERAL INFORMATION:
TATHIGANT ROBISON, Keith E.
TITHE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
TITHE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
PRIOR APPLICATION NUMBER: US/09/833,381
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 gercasececasecesses and a second contraction of the second of the sec
9 GGGGTCAGGCCCCAGCGCGGGAAGCGCCCCAAGAGCGCGCGAAACCTTCTCCACACACC 68
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Pred. No. 11;
0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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59.5%; Pred. No. 10;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                           195 CTCAAGTCGCACTCCCGACGC 175
                                                                                                                                                                                                   69 TTCCAGGCATTTGCCCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.5%;
Best Local Similarity 57.5%;
Matches 50; Conservative
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Matches 47; Conservative
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514
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                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: LI, ET AL.

TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,

STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                        DB 14; Length 2483;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPE. 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFFWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,891
FILING DATE: 23-Dec-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FERRARO, GRECORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/009,492
FILING DATE: CUNKROWN-
PAPLICATION NUMBER: 08/464,340
FILING DATE: June 5,1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      ch 27.5%; Score 27.8; D
1 Similarity 57.5%; Pred. No. 10;
50; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 eccecechácerecrecececerata 541
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                                                                                                                             TOPOLOGY: LINEAR MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                      65 ACCCTTCCAGGCATTTGCCCGCCGCGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2483 BASE PAIRS
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10325891
Publication No. US20030092895A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744
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                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
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ZIP: 07068
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
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Best Local Similarity
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Best Local Similarity
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    117 GGCGCTCGGCGCCTGCTGCTGCTCCTTCCCCGCGCACGATGCCGTGTCCACCGCT
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION WIMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SEQ ID NO 2344
LENGTH: 2323
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
FRCCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10143002
Publication No. US20020132775A1
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Potassium Channel Protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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REFERENCE/DOCKET NUMBER: 325800-310
TELECOMMUNICATION INFORMATION:
TELEPRONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27.8; DB
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/102,493
FILING DATE: «Unknown»
APPLICATION NUMBER: US/08/468,533
FILING DATE: 6 JUNE 1995
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/143,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IEM PS/2 OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                           ; Sequence 2344, Application US/10108260A; publication No. US20040005560A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CECCHI, STEWART
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.
                                                                             57 GTCCAGGCTCTGTCCTCC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
27.5%;
Best Local Similarity 74.5%;
Matches 35; Conservative
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STATE: NEW JERSEY
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장 <u>원</u>

Dp

Search completed: May 7, 2004, 17:35:50 Job time : 454.502 secs

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Sequence 649, Applemence 3, Appli Sequence 31, Appli Sequence 811, Applemence 111, Applemence 1262, Applemence 15295, Applemence 15295, Applemence 2, Appli Sequence 2, Appli Sequence 2, Appli
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US-09-833-381-649
US-08-464-340A-3
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US-09-489-039A-831
US-09-252-991A-15295
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Sequence 11, Application US/09790045

; Sequence 11, Application US/09790045

; Patent No. 649210

; GENERAL INCRMATION:

; APPLICANT: Hasebe, Akira

APPLICANT: Hasebe, Akira

APPLICANT: Hache, Mitsuo

; TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia Solanacearum

; PATENT APPLICATION NUMBER: US/09/790,045

; FILE REFERENCE: NANPIOBUS

; CURRENT APPLICATION NUMBER: US/09/790,045

; CURRENT FILING DATE: 2001-02-21

; NUMBER OF SEQ ID NOS: 14

; SEQ ID NO 11

LEMOTH: 884
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                                                                                                                   Sequence 1288, A Sequence 11208, A Sequence 11208, A Sequence 11046, A Sequence 15756, A Sequence 10971, A Sequence 10, Appl Sequence 10, Appl Sequence 1556, A Sequence 1556, A Sequence 1568, A Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli
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US-10-222-577-11/c
US-10-222-577-11/c

Sequence 11, Application US/10222577

Patent No. 6538125

APPLICANT: Hasebe, Akira

APPLICANT: Hasebe, Akira

APPLICANT: Horita, Mitsuo

TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia

Patent No. 6538125

TITLE OF INVENTION: Solanacearum

FILE REFERENCE: NANPLOBUS

CURRENT APPLICATION NUMBER: US/10/222,577
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STREET: 6 DELL
CITY: ROSELAND
STATE: NEW JERSEY
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Sequence 11. Application US/1022578

Patent No. 657007

GENERAL INFORMATION:
APPLICANT: Hasebe, Akira
APPLICANT: Hasebe, Akira
APPLICANT: Horita, Mitsuo
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia
PILE REFERENCE: NANP108US
TITLE OF INVENTION: Solanacearum
FILE REPERENCE: NANP108US
CURRENT APPLICATION NUMBER: US/10/222,578
CURRENT APPLICATION NUMBER: US/09/790,045
FRIOR APPLICATION NUMBER: US/09/790,045
FRIOR APPLICATION NUMBER: US/09/790,045
FRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SOFTHARE: Patentin version 3.0

LENGTH: 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.9%; Score 28.2; D
59.3%; Pred. No. 7.2;
iive 0; Mismatches
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/790,045
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 11
LENGTH: 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crcaagrogeactocogacec 175
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Patent No. 6672186
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ORGANISM: Ralstonia solanacearum
                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TICCAGGCATITGCCCGCCGC
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APPLICANT: Robison, Keith E.
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Matches 48; Conservative
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; LOCATION: (44)...(865)
US-10-222-578-11
                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (44)...(865)
US-10-222-577-11
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Best Local Similarity
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US-09-833-381-649
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TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 412
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Patent No. 5710019
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                            37; Indels
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ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                           Score 27.8; DB Pred. No. 8.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,340A
FILING DATE: June 5,1995
CLASSIPTECATION DATA:
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
ATTORNAY/AGENT INFORMATION:
NAME: FERRARO, GREGGRY D.
REGISTRATION NUMBER: 3,134
REFERRANCE/DOCKET NUMBER: 3,25800-415
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 cacciccaagreracercicceccada 230
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57.5%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
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Gaps

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Length 1665; Indels

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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 14;
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                         FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 831
LENGTH: 1665
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EARLIER APPLICATION NUMBER: 60/049,885

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING
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R APPLICATION NUMBER: 60/048,880
R FILING DATE: 1997-06-06
R PILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,020
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R APPLICATION NUMBER: 60/048,884

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,894

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,971

R APPLICATION NUMBER: 60/048,964

R APPLICATION NUMBER: 60/048,964

R R PILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
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APPLICATION UNMBER: 60/048,876
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA; CREDSiella pneumoniae; OKGANISM: Klebsiella pneumoniae
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1 Similarity 54.5%;
55, Conservative
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Best Local Similarity
                TITLE OF INVENTION:
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                           37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9408449A
GENERAL INFORMATION:
APPLICANT: L1, ET AL.
TITLE OF INVENTION: Potassium Channel Protein 1 and 2
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
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57.5%; Pred. No. 11;
cive 0; Mismatches
                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCCCCAGGCTGCTGCCCGCTGTGA 541
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/0844.
FILING DATE: SUBMITTED HERBMITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 831, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2483 BASE PAIRS TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 57.5
Matches 50; Conservative
                                 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACII
STRANDEDNESS: SINC
TOPOLOGY: LINEAR
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-489-039A-831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515
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                                      Matches
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US-09-252-991A-15544/c

is equence 15544, Application US/09252991A

sequence 15544, Application US/09252991A

patent No. 6551795

GENERAL INFORMATION:

APPLICATION

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

AREOGRAPHICATION UNMERR: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15544

LENGTH: 1326
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US-09-252-991A-15544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.3%; Score 26.6; DB 4; Length 599; Best Local Similarity 54.6%; Pred. No. 21; Matches 53; Conservative 0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                           GENERAL INCORATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TAPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARR: Patent.pm
SEQ ID NO 2262
LENGTH: 599
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                                       Sequence 2262, Application US/09621976 Patent No. 6639063
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: CDS
) LOCATION: 216..368
US-09-621-976-2262
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NAME/KEY: unsure
LOCATION: (92)
                     JS-09-621-976-2262
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                                                                                                                                                                                   EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049, 374
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
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LOCATION: (1999)
CTHER INFRAMITION: n equals a,t,g, or US-09-205-258-171
                                                                                                             APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,892
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 171
LENGTH: 2003
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.1%; Score 26.4; DB 3; Length 742; Best Local Similarity 59.2%; Pred. No. 25; Matches 45; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,848 FILING DATE: 28-MAY-1998 CLASSIFICATION: 435
141 AGTCCGCCGATCAGCAGCGGCGCCATCAGGGA 172
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSS:
ADDRESSEE: MEDLEN & CARROLL, ILP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ASKARI, FREDERICK K.
TITLE OF INVENTION: IMPROVED VECTORS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLI
                                                                                                                          Sequence 2, Application US/09085848
Patent No. 6171855
GENERAL TORNATION:
APPLICANT: ASSTARI, FREDERICK K.
TITLE OF INVENTION: IMPROVED VECTORS
                                                                                                                                                                                                                                                                                                                                                                CITY: SAN FRANCISCO
STATE: CALLFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-562-616-2/c; Sequence 2, Application US/09562616; Patent No. 6599744; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 cGGACACTIGICCCCC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CAGGCATTTGCCCGCC 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                              RESULT 13
US-09-085-848-2/c
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US-09-252-991A-13956

i Sequence 13956, Application US/09252991A

patent No. 6551795

GENERAL INFORMATION:
APPLICATION:
APPLICATION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR SEQ ID NOS: 33142

SEQ ID NO 13956
                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1253)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-15295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 CCTGGGGGTCAGGCCCCAGCCGGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCCAC 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Score 26.6; DB 4; Length 1.
58.0%; Pred. No. 24;
tive 0; Mismatches 34; Indels
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                                                                                                    Sequence 15295, Application US/09252991A
Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th 26.1%;
| Similarity 55.4%;
| Similarity 55.4%;
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Best Local Similarity 58.0
Matches 47; Conservative
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Best Local Similarity
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                                                                                    US-09-252-991A-15295
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US-09-252-91A-13604/c

US-09-252-91A-13604, Application US/09252991A

Sequence 13604, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/62,616
FILING DATE: 01-May-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION NUMBER: US/09/085,848
ATYORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UM-03338
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8318
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | IENGTH: 742 base pairs | IENGTH: 742 base pairs | TYPE: nucleic acid | STRANDEDNESS: double | TOPOLOGY: linear | MOLECUE TYPE: chter nucleic acid | BESCRIPTION: /desc = "DNA" | SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-562-616-2
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13604
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LENGTH: 2103
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68 CTTCCAGGCATTTGCCCGCCGCGATTCAGAGA 99

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1182 AGTCCGCCGATCAGCAGGCGCGCATCAGGGA 1151
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Search completed: May 7, 2004, 15:44:40 Job time : 57.7167 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                   Copyright
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- nucleic search, using sw model OM nucleic Run on:

7, 2004, 11:56:28 , Search time 206.335 Seconds (without alignments) 2079.475 Million cell updates/sec

1 ggaacctggggggtcaggccc........cccgccgcgattcagagagc 101 US-10-071-411A-1_COPY_950_1050 Perfect score: Sequence: Title:

3373863 seqs, 2124099041 residues Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table: Searched:

6747720

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries

geneseqn2001as:*
geneseqn2001bs:*
geneseqn2002s:*
geneseqn2003as:* N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:* geneseqn2003bs:*geneseqn2003cs:* geneseqn2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	G	Abt11173 Human 5-1	Abt11114 Human 5-1		Abk31177 Signal tr	Abl70132 Chemicall	Abl32116 Human imm	Abk31176 Signal tr	Abl70131 Chemicall	Abk84481 Human cDN	Add14691 Human src	Aal50815 Human can	Abz59005 Human onc	Abz52368 Aspergill	Abz58996 Human onc	Abz58995 Human onc	Aac98960 Human pan	Abk15293 Ralstonia	Aba99469 Actinopla	Aat77840 Human mel	Aat12462 Human K+	Aav04874 cDNA segu	Adc99154 Human mat	Adas7655 BAC fragm
SOMETHIES		ABT11173	ABT11114 A	ABL32117 A	ABK31177 A	ABL70132 A	ABL32116 A	ABK31176 P	ABL70131 A	ABK84481	ADD14691	AAL50815	ABZ59005	ABZ52368 p	ABZ58996	ABZ58995	AAC98960	ABK15293	ABA99469	AAT77840	AAT12462 P	AAV04874	ADC99154	ADA57655 P
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	Length DB	168174	168273	13249	13249	13249	13249	13249	13249	44147	44147	33737	926	99	3761	10735	381	890	38064	1735	2483	2483	2483	4456
æ	Query Match	88.1	88.1	54.5	54.5	54.5	42.8	42.8	42.8	29.7	29,7	29.1	28.7	28.7	28.7	28.7	28.1	27.9	27.7	27.5	27.5	27.5	27.5	27.5
	Score	89	89	55	55	55	43.2	43.2	43.2	30	30	29.4	29		29	29	28.4	28.2	28	27.8	27.8	27.8	27.8	27.8
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Ada41527 Human sec	Adc74634 Human sec	Aas26792 Human gen	Ada57654 BAC fragm	Ada41526 Human sec	Abx74141 Human nov	Adc74633 Human sec	Aai59411 Human pol	Aak91239 Human dig	Aak91240 Human dig	Aba06675 Human cDN	Aas31605 cDNA enco	Abv84012 Human pol	Add47395 Rat gene	Aca35947 Prokaryot		Abg53010 Oligonucl	Aax04400 Human sec	Aav84571 Human sec	Aba83354 Human sec	Ach04855 Novel hum	Acd44665 Human cDN
ADA41527	ADC74634	AAS26792	ADA57654	ADA41526	ABX74141	ADC74633	AAI59411	AAK91239	AAK91240	ABA06675	AAS31605	ABV84012	ADD47395	ACA35947	ABQ53011	ABQ53010	AAX04400	AAV84571	ABA83354	ACH04855	ACD44665
7	6	4	7	7	7	σ	4	4	4	4	4	ø	σ	7	9	9	7	N	4	œ	œ
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27	27	27	27.5	27	27	27	27	27	27	56	26	26	26	26	26	26	26	26	26	26	26
27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.4	27.4	27.4	27.2	27.2	27.2	27.2	27.2	27	27	27	27	27	27	27
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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Human, polymorphic region, 5-lipoxygenase, 5-LO gene, asthma, bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, sarcoidosis, hemuatoid arthritis, scleroderma, lupus, non-allergic thinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, atopic, contact dermatitis, forensic medicine, paternity testing, enzyme,
                                                                    Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
                 ABT11173 standard; DNA; 168174 BP.
                                                   (first entry)
                                                   05-DEC-2002
                                  ABT11173;
RESULT 1
         ABT11173
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07-FEB-2002; 2002WO-US003546. WO200262825-A2. Homo sapiens. 15-AUG-2002.

(MILL-) MILLENNIUM PHARM INC. Barnes G, Meyer J;

WPI; 2002-627522/67.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma.

Disclosure; Fig 4; 290pp; English.

The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the

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present invention are useful for diagnosing and/or prognosing disorders associated with an aberrant inflammatory response such as asthma, bronchitis, simusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, soleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing.
                                                                                                                                                                                                                                        gene of the invention
                                                                                                                                                                                                                                           lipoxygenase (5-LO)
          8888888888888
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Sequence 168174 BP; 46808 A; 36442 C; 36942 G; 46474 T; 0 U; 1508 Other;

1, Length 168174; Indels Score 89; DB 6; Le:
Pred. No. 7.6e-17; 0; Mismatches 88.1%; 99.0%; Conservative Similarity Best Local Sim: Matches 100; Query Match

1 GGAACCTGGGGGCTCAGGCCCCAGCCGCGCAAGCGCCCCAGGAGCGCGCGAAACCTTCT

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RESULT 2

ABT11114 standard; DNA; 168273

BP

(first entry) 05-DEC-2002 ABT11114;

Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.

Human, polymorphic region, 5-lipoxygenase, 5-LO gene, asthma, bronchitis, sinusitis, ulcerative colitis, nephritis; amyloidosis; sarcoidosis; hebumatoid arthritis; scleroderma, lupus; non-allergic rhinitis; polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;

Homo sapiens.

WO200262825-A2

15-AUG-2002

07-FEB-2002; 2002WO-US003546

08-FEB-2001; 2001US-0267515P 21-AUG-2001; 2001US-0314248P

(MILL-) MILLENNIUM PHARM INC

Meyer J; Barnes G, WPI; 2002-627522/67

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma.

Disclosure, Fig 2; 290pp, English.

comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the present invention are useful for diagnosing and/or prognosing disorders The invention relates to an isolated human nucleic acid molecule

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

Claim 1; SEQ ID NO 90; 32pp + Sequence Listing; German.

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      bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic thinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the aams species for use in forensic medicine and paternity testing. This polymucleotide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS, epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemically modified gene, useful for associated with abnormal cytosine
                                                                                                                                                              Sequence 168273 BP; 46834 A; 36467 C; 36966 G; 46498 T; 0 U; 1508 Other;
                                                                                                                                                                                                                                                                                             167418 GERACCTGGGGGTCAGGCCCCGGGGAAGC-CGCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                                                 1 GGAACCTGGGGGTCAGGCCCCCAGCGGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic;
such as asthma,
                                                                                                                                                                                               Length 168273;
                                                                                                                                                                                                                                                                                                                                                                 167477 ccacaccerrecagecarrrecececececearreagage 167517
                                                                                                                                                                                                                                                                                                                                61 CCACACCCTTCCAGGCATTTGCCCGCGCGATTCAGAGAGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune system associated gene SEQ ID NO: 90.
response
                                                                                                                                                                                             88.1%; Score 89; DB 6; 1
99.0%; Pred. No. 7.6e-17;
ive 0; Mismatches 0;
associated with an aberrant inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fragment of of diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL32117 standard; DNA; 13249
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2000DE-01043826.
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                                                                                                                                                                                                                                Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-130909/17
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A,
                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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specification, but was obtained in electronic format directly from the European Patent Office

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Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;

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Gaps

1;

Length 13249; 20; Indels

Score 55; DB 6; Pred. No. 7.8e-07 0; Mismatches

54.5%;

Query Match
Best Local Similarity 78.0.
Best Total Similarity 78.0.

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                                                                                                                                                                                            9089 AACCTAAAAATCAAACCCCAACCGCGAAAAC-CGCCCAAAAACGGGGGAAACCTTCTCC 9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, bydrogen sulphite or disclosed are oligonucleotides and/or DNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31159-ABK31545 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                              3 AACCTGGGGGTCAGGCCCCAGCCGCGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCC
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal transduction associated gene modified complementary DNA #10.
 psoriasis and inflammatory/ulcerative bowel sequence is a gene of the invention
                                                                                                                            1;
                                                      Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                                                                         Length 13249;
                                                                                                                            20; Indels
                                                                                                                                                                                                                                                                  9030 ACACCCTTCCAAACATTTACCCGCGCGATTCAAAAAC 8992
                                                                                                                                                                                                                                 63 ACACCCTTCCAGGCATTTGCCCGCGCGATTCAGAGAGC 101
                                                                                         Score 55; DB 6;
Pred. No. 7.8e-07;
                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                     54.5%;
78.8%;
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                      Local Similarity 78.8 les 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPIG-) EPIGENOMICS AG.
rheumatoid arthritis,
diseases. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200200926-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                             ABK31177;
                                                                                         Query Match
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is constant of the chemically modified DNA of genes associated with cell carpaning, as well as a soligonucleotides and/or DNA-oligoners for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided with enivention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL7011-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                    9089 aaccraaaarcaaaccccaaccccaaaaaac-ccccaaaaacccccaaaaaccccaaaacccrrcrcc 9031
    62
                                                                                                                                                                                                                                                                                                                                                                                            signalling; cytosine methylation; cell signalling disease; cancer; rx; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
3 AACCTGGGGGTCAGGCCCCAGCGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCC
                                                                                                                                                                                                                                                                                                                                                   Chemically treated cell signalling DNA sequence complementary to#11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 22; 24pp + Sequence Listing; English.
                                                                                                        9030 ACACCCTTCCAAACATTTACCCGCCGCGGATTCAAAAAAC 8992
                                                                                63 ACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K;
                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                         ABL70132 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2001; 2001WO-EP007471.
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                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                           01-JUL-2002
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                                                                                                                                                                                                                                                                    ABL70132;
                                                                                                                                                                                                                                                                                                                                                                                                                  tumour;
                                                                                                                                                                                                     ABL70132,
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chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebuxaemia, Alzheimer's disease, Alzb. epilepsy, neurofibromatosis, rheumatoid arthritis, psociasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiartestelocic; antianaemic; cytostatic; nototropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologica; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthmatory; cancer; eye disease; arteriosclerosis; anamic, actual manalory; cancer; eye disease; arteriosclerosis; and contempoloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified gene, useful f
with abnormal cytosine
                                                                                                             9089 AACCTAAAAATCAAACCCCAACCGCGAAAAAC-CGCCCAAAAAAGGGGGGAAACCTTCTCC
                                                                                  3 AACCTGGGGGTCAGGCCCCAGGGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCC
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
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               Length 13249;
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Pred. No. 0.0026;
0; Mismatches 28; Indels
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 89; 32pp + Sequence Listing; German.
                                                                                                                                                                                   9030 ACACCCTTCCAAACATTTACCCGCCGCGATTCAAAAAC 8992
                                                                                                                                                    63 ACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAGC 101
                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 89.
                                                 20;
               Score 55; DB 6;
Pred. No. 7.8e-07;
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 54.5%; Scor. 78.8%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                         (first entry)
Query Match
Best Local Similarity 70...
Rest Local Similarity 70...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation.
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disculphite.

Also disclosed are oligomorlectides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method contained associated with signal transduction. The genes, and a method genes associated with signal transduction. The genemic DNA, e.g. cell contained from cells or cellular components which contain DNA, e.g. cell contained from cells or cellular components which contain DNA, e.g. cell contain, heart, prostate, lung, breast or liver, histologic object slides, brain, heart, prostate, lung, breast or liver, histologic object slides, cuseful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed support the printed of the contained th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4159 GGAATTTGGGGGTTAGGTTTTAGTCGCGGGAAG-TCGTTTAGGAGCGCGCGAAATTTTTT 4217
                                                                                                                                                                                                                                                                                                                                                                                                         Human, signal transduction associated gene, cytosine methylation state, CpG island, signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43.2; DB 6; Length 13249;
Pred. No. 0.0026;
0; Mismatches 28; Indels 1;
                                                4218 TRATATTTTTAGGTATTTGTTCGTCGCGATTTAGAGAG 4257
61 CCACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAG 100
                                                                                                                                                                                                                                                                                                                                                        Signal transduction associated gene modified DNA #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 19; 24pp; English.
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                                                                                                                                                                                         BP.
                                                                                                                                                                                         ABK31176 standard; DNA; 13249
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71.0%;
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01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 71.0
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                               ABK31176
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                                                                                                                                     RESULT 7
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Gaps

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DB 6; Length 13249;

71.0%;

Local Similarity 71.0 es 71; Conservative

Matches

d à

Query Match

4217

4159 GGAATTTGGGGGGTTAGGTTTTAGTCGCGGGAAG-TCGTTTAGGAGCGCGCGAAATTTTTT

GGAACCTGGGGGGTCAGGCCCCAGCGGGGGAAGCGCCCCAGGAGCGCGCGGAAACCTTCT

Tue May 11 11:56:46 2004

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as a method which is checting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL/1011-ABL/10626 represent chemically pre-treated genemic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sepecification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4159 GGAATTIGGGGGTITAGGTTITTAGICGCGGGAAG-ICGTITAGGAGCGCGCGAAATTITTI 4217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell signalling; cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genemic sequences of genes associated with cell signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 21; 24pp + Sequence Listing; English.
                                        4218 TTATATTTTTTAGGTATTTGTTCGTCGCGATTTAGAGAG 4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CCACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAG 100
61 CCACACCCTTCCAGGCATTGCCCGCCGCGATTCAGAGAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemically treated cell signalling DNA sequence#11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                             ABL70131 standard; DNA; 13249 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 71.0
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; cytostatic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified.
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                                                                                                                                                                        RESULT 8
ABL70131
ABL
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4218 TTATATTTTTTAGGTATTTGTTCGTCGCGATTTAGAGAG 4257

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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contexting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue or sterile inflammatory disease using the gene expression of subject to a pathogen or sterile inflammatory disease using the gene expression of the seponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammatory disease, by contracting a tissue having inflammation with an agent that modulates the expression of gene (s) from GS, where the is useful for detecting GCA; M2 is useful for modulating GA, M3 is useful to sepecially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammation in a tissue, M4 is useful for modulating GA, M3 is useful (especially chronic) in a tissue, an allergic response in a subject (correcting an inflammation in a tissue, M4 is useful for detecting an inflammation of exposure of a subject to a pathogen or sterile inflammation disease, correcting an inflammation disease, correcting an inflammation in a tissue, M4 is useful for detecting an inflammation of exposure of a subject to a pathogen or sterile inflammatory disease.

C exposure of a subject to a pathogen or sterile inflammatory disease (e.g. cardiac reperfusion injury, renal reperface of the correction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
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                                                                                                                                                                                                                                                       Human; ss; granulocytic cell; DNA chip; bacterial infection, viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephitis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARBS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                           Human cDNA differentially expressed in granulocytic cells #1052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1052; 114pp; English.
                                                 ABK84481 standard; cDNA; 44147 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beazer-Barclay Y, Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2001; 2001WO-US030821.
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-435328/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2000;
                                                                                                                                                       14-AUG-2002
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                                                                                                     ABK84481;
                        ABK84481/c
RESULT 9
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or polypeptides that predict the sensitivity or

polynucleotides

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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase activity or cells, comprising obtaining a sample of cells, modulating the activity of cells, comprising obtaining a sample of cells, determining whether the cells for modulate the cells appress a plurality of markers and correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polynucleotides and polypeptides that predict compound sensitivity or resistance of cells associated with a disease state, comprising the expression pattern of cell innes to one or more compounds, analysing the expression pattern of
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss.
                                                                                                                                                                                                         68
expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                       9 GGGGTCAGGCCCCAGGGGGGAAGGGGCGCCCAGGAGCGCGCGAAACCTTCTCCACACCC
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein
                                                                                             Other;
                                                                                                                                                                      ;
                                                                                         Sequence 44147 BP; 9813 A; 11709 C; 11789 G; 10833 T; 0 U; 3
                                                                                                                               Score 30; DB 6; Length 44147;
Pred. No. 26;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human src biomarker polynucleotide SEQ ID NO:85.
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                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; SEQ ID NO 85; 139pp; English.
                                                                                                                                                                                                                                                                               69 TTCCAGGCATTTGCCCGCGCGATTC
                                                                                                                                                                                                                                                                                                                                                                                                            ADD14691 standard; cDNA; 44147 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee FY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                               29.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2002; 2002US-0350061P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine kinase pathways.
                                                                                                                                                                    51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang F, Fairchild CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-636735/60
                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD14691;
                                                                                                                                   Query Match
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microarray of polynucleotides or polypeptides, and selecting

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            resistance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and polypeptides have cytostatic activities, and can be used in gene therapy. The polynucleotides are expostatic activities, and can be used in gene therapy. The polynucleotides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nter-aided statistical method for predicting cancer, applicable in
therapy for evaluating cancer malignancy with data for use in drug
                                                                                                                                                                                                                                                                                                                                                    9 GGGGTCAGGCCCCCAGGGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACC
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                    Sequence 44147 BP; 9813 A; 11709 C; 11789 G; 10833 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene therapy; cancer status prediction; cancer; ds; cancer malignancy evaluation; drug design; antisense nucleic acid
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0
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                                                                                                                                                                                                                                                                         29.7%; Score 30; DB 9; Length 44147; 59.3%; Pred. No. 26; ive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 132-152; 182pp; Japanese.
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(HISF ) HITACHI SOFTWARE ENG CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                69 TTCCAGGCATTTGCCCGCCGCGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
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06-APR-2001; 2001JP-00108503.
02-AUG-2001; 2001JP-00234807.
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                                                                                                                                                                                                                                                                                         Local Similarity 59.3
nes 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200272828-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    design.
                                                                                                                                                                                                                                                                                                               Matches
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fermentation; fungus; industrial; EST;

expressed sequence tag; gene; ss.

Aspergillus oryzae.

WO200279476-A1.

Aspergillus oryzae;

2002WO-IB000890.

22-MAR-2002;

10-OCT-2002

Aspergillus oryzae polynucleotide SEQ ID NO 1481

28-MAR-2003

ABZ52368;

ABZ52368 standard; cDNA; 990 BP.

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ABZ52368/c
                      RESULT 13
                                           ö
                                                                                                                 8876 GGCTCAGGCCCCTGCCAGACGCCCCCAGACGCCCCCAGACGCCCCTCCACCCTCCT 8817
                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CCTGGGGGTCAGGCCCCCAGCGGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCCAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncosuppressive; apoptotic; p53; p73; cytostatic; gene therapy; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                       10 GGGTCAGGCCCCAGCCGCGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCCACACCCT
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to oncosuppressive polypeptides and encoding polynuclectides. The oncosuppressive gene is involved in apoptotic process and is regulated by p53 and p73. The oncosuppressive polynuclectides are useful for preparing a medicament for treating tumour. The present sequence represents a human oncosuppressive gene (DRAGO) fragment regulating the expression of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oncosuppressive polypeptide, useful for preparing a medicament
for use in drug design (e.g. antisense nucleic acids for use in therapy to treat cancer). The present DNA sequence represents a nucleic acid of the invention
                                          Sequence 33737 BP; 8084 A; 9254 C; 8733 G; 7663 T; 0 U; 3 Other;
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                                                              Length 33737;
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Pred. No. 33;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 956 BP; 104 A; 371 C; 353 G; 128 T; 0 U; 0 Other;
                                                                                  Indels
                                                                                  21;
                                                              DB 6;
                                                            Score 29.4; DE Pred. No. 37; 0; Mismatches
                                                                                                                                                                                                                                                                                  Human oncosuppressive gene (DRAGO) fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 42; 42pp; English,
                                                                                                                                                                                                                     ABZ59005 standard; DNA; 956 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-2001; 2001IT-MI001465.
                                                             Match 29.1%;
Local Similarity 66.7%;
les 42; Conservative
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                                                                                                                                                                                                                                                                                                               DRAGO; human; gene; ds
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Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treating tumors.
                                                                                                                                               70 TCC 72
                                                                                                                                                                                                                                                                                                                                                      WO2003006498-A2
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ5088-ABZ56893), which are expressed by a fungus under specific outlure conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising progress of fermentation and the growth conditions of monitoring the especially of Aspergillus oryzes which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                              monitoring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GCCCCAGCCGCGCGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACCTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467 GTCCCAGGCGCCGGAAGCAGGCACCGCAGCCTGCCAAACCTGCCGCACCATCTGCGACGG
                                                                                                                                                                                                                                                                                                                                    Detection of expression of specific Aspergillus genes for monitorir fermentation and growth conditions of the fungus, using DNA probes.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1481; 48pp + Sequence Listing; Japanese.
                                                                                                                                                                                  Horiuchi Abe K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.7%; Score 29; DB 7; Length 990; 58.8%; Pred. No. 33; ive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 990 BP; 247 A; 262 C; 243 G; 235 T; 0 U; 3 Other;
                                                                                                                                                                               Machida M, Akita O, Kashiwagi Y, Kitamoto K,
Takeuchi M, Kobayashi T, Kitamoto N, Gomi K,
                                                       INST ADVANCED IND SCI & TECHNOLOGY
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                                                                                       (NARE-) NAT RES INST BREWING.
(NORQ ) NAT FOOD RES INST MIN AGRIC.
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30-MAR-2001; 2001JP-00098371.
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                                        Oncosuppressive; apoptotic; p53; p73; cytostatic; gene therapy; tumour; DRAGO; human; gene; ds.
                                                                                                                                                                                                                                                 New oncosuppressive polypeptide, useful for preparing a medicament for treating tumors:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                               The invention relates to oncosuppressive polypeptides and encoding polynucleotides. The oncosuppressive gene is involved in apoptotic process and is regulated by p53 and p73. The oncosuppressive polynucleotides are useful for preparing a medicament for treating (undur. The present sequence represents a human oncosuppressive gene (DRAGO) fragment
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Pred. No. 38;
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                      Human oncosuppressive gene (DRAGO) fragment
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                                                                                                                                                                                                                                                                                           Claim 3; Page 37-38; 42pp; English
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                                                                                                                                              09-JUL-2002; 2002WO-EP007625.
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28.7%;
Best Local Similarity 58.8%;
Matches 50; Conservative
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ABZ58995
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                                                                                                                                                                                 New oncosuppressive polypeptide, useful for preparing a medicament for
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                                                       Broggini M, D'incalci M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.7
Best Local Similarity 58.8
Matches 50; Conservative
(NOVU-) NOVUSPHARMA
                                                                                                                      WPI; 2003-221715/21
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                                                                                                                                                                                                                        treating tumors
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 O PB 3 11 O	OM nucleic - nuc	nucleic search, using sw model
US-10-071-411A-1_COPV_950_1050 1: 103 Tagaacctgggggtcagggccagggccccccgccgcgattcagaggcccc.table: IDENTITY NUC Gapop 10-0 , Gapext 1.0 1: 3470272 seqs, 21671516995 residues	:uo	7, 2004, 13:24:59 ; Search time 1052.91 Seco (without alignments) 4157.648 Million cell
table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 short of hits satisfying chosen parameters: DB seq length: 200000000 Cessing: Minimum Match 0% Maximum Match 0% Maximum Match 0% Isting first 45 summaries GenEmbl:* 1 gb ba:* 1 gb la:* 2 gb ln:* 4 gb om:* 5 gb ph:* 8 gb ph:* 10 gb ro:* 11 gb pt:* 12 gb pr:* 13 gb ln:* 14 gb or:* 15 gb pr:* 16 gb pr:* 17 gb ph:* 18 em hi:* 19 em n:* 11 gb cter:* 12 gb gr:* 12 gb gr:* 13 gb ro:* 14 gb or:* 15 em hi:* 16 em n:* 17 em hi:* 18 em n:* 19 em n:* 21 em or:* 22 em or:* 23 em ph:* 24 em ph:* 25 em ph:* 26 em ro:* 27 em co:* 27 em co:* 28 em htg other:* 30 em htg other:* 31 em htg ph:* 32 em htg orie:* 33 em htg orie:* 34 em htg orie:* 35 em htg orie:* 36 em htg orie:* 37 em htg orie:* 38 em htg orie:* 39 em htg orie:* 30 em orie:* 40 em htg o	score:	_COPY_950_1050 aggccccccgccgcgattcagaggc
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mber of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 0 Cessing: Minimum Match 09* Listing first 45 summaries GenEmbl:* 1: 9b ba:* 2: 9b_ntg:* 4: 9b_om:* 5: 9b_pt:* 7: 9b_pt:* 9: 9b_pt:* 11: 9b_pt:* 12: 9b_pt:* 13: 9b_un:* 14: 9b_vi:* 14: 9b_vi:* 15: em_ba:* 16: em_fun:* 17: em_hum:* 18: em_pi:* 21: em_or:* 22: em_or:* 23: em_pi:* 24: em_or:* 25: em_pi:* 26: em_vi:* 27: em_or:* 28: em_htg_inv:* 29: em_vi:* 21: em_or:* 21: em_or:* 22: em_or:* 23: em_htg_inv:* 24: em_htg_inv:* 25: em_htg_inv:* 26: em_vi:* 27: em_htg_inv:* 28: em_htg_inv:* 29: em_vi:* 30: em_htg_inv:* 31: em_htg_inv:* 32: em_htg_inv:* 33: em_htg_inv:* 34: em_htg_inv:* 35: em_htg_inv:* 36: em_htg_inv:* 37: em_htg_inv:* 38: em_htg_inv:*	Searched:	seqs, 21671516995 residue
DB seq length: 0 DB seq length: 2000000000 Cessing: Minimum Match 99% Listing first 45 Listing first 45 1: gb_ba:* 2: gb_htg:* 3: gb_ln:* 4: gb_pr:* 6: gb_pat:* 7: gb_pr:* 11: gb_gr:* 11: gb_gr:* 11: gb_gr:* 12: gb_gr:* 12: gb_gr:* 13: gb_gr:* 14: gb_gr:* 15: gb_gr:* 16: em_fun:* 17: gb_gr:* 18: em_ba:* 18: em_pr:* 19: em_mu:* 19: em_mu:* 19: em_mu:* 19: em_mu:* 19: em_mu:* 19: em_mu:* 19: em_pr:* 21: em_pr:* 22: em_pr:* 23: em_pr:* 23: em_pr:* 24: em_pr:* 25: em_pr:* 26: em_pr:* 27: em_gr:* 28: em_pr:* 29: em_pr:* 29: em_pr:* 29: em_htg_inv:* 30: em_htg_inv:* 31: em_htg_inv:* 32: em_htg_inv:* 33: em_htg_inv:* 34: em_htg_inv:* 35: em_htg_inv:* 36: em_htg_inv:* 37: em_htg_inv:* 38: em_htg_inv:* 38: em_htg_onus:*	number of	satisfying chosen parameters:
cessing: Minimum Match 09* Maximum Match 99* Listing first 45 1	DB seq DB sed	
GenEmbl:* 1: gb ba:* 2: gb nr:* 4: gb nr:* 5: gb nr:* 6: gb pat:* 7: gb pat:* 10: gb pr:* 11: gb pr:* 11: gb pr:* 12: gb nr:* 13: gb nr:* 14: gb nr:* 15: em ba:* 16: em fun:* 17: em hum:* 18: em pr:* 22: em or:* 23: em pr:* 24: em pr:* 25: em pr:* 26: em ri:* 27: em pr:* 28: em pr:* 29: em vi:* 29: em vi:* 31: em htg num:* 31: em htg num:* 33: em htg num:* 34: em htg num:* 35: em htg num:* 36: em vi:* 37: em htg num:* 38: em htg num:* 39: em vi:* 39: em vi:* 39: em vi:* 39: em htg num:*	Post-processing:	Minimum Match 0% Maximum Match 99% Listing first 45
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AL731567 129266 bp DNA linear PRI 20-JUN-2002

NO Human DNA sequence from clone RP11-67C2 on chromosome 10, complete sequence

Sequence AL731567 AC010865

NAT731567 AC010865

HTG.

Homo sapiens (human)

HOMO sapiens (human)

Exaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mintehead, S.

Direct Submission ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AL731567 LOCUS DEFINITION

ALIGNMENTS

REFERENCE AUTHORS TITLE

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Castellano, K., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Castellano, K., Dewar, K., Collymore, D., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Perreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Horland, J., Grant, G., Hagos, B., Haedrord, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGwran, R., McLaughlin, J., Melrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollaray, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stofanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. Old, W. Submission

N. Submissio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 2.9 in Q20 bases; agarose-fp Quality coverage: 3.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 151 bp in length
gap of 100 bp
contig of 1509 bp in length
gap of 100 bp
contig of 1209 bp in length
gap of 100 bp
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gap of 100 bp
contig of 2341 bp in length
gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1860:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4820:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6174:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7417:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9158:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1760:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3069:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15671:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18182:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                Cambridgeshire, CBIO 15A, WE E-mail enquiries:

Nummerer (11-17202) Wellcome requests: clonerequest@sanger.ac.uk

On Jun 21, 2002 this sequence version replaced gi:21213582.

Draft Sequence Produced by Genome Therapeutics Corp, 100 Beaver

Street, Waltham, MA 02453, USA

http://www.genomecorp.com

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone ame. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

10); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one Mil subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em; EMBL; Sw;,

SMISSPROT; TT: TREMBL; Wp;, WORMPEP; Information on the WORMPEP

database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 10, constructed by the Sanger Centre Chromosome 10

Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/ChiO

RPII-6702 is from the library RPOI-111 constructed by the group of

Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACULL879 16-0654 bp DNA linear HTG 16-WAR-2000
Homo sapiens clone RP11-16P14, WORKING DRAFT SEQUENCE, 30 unordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160654)
                            Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGAACCTGGGGGTCAGGCCCCAGCCGCGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCT
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Pred. No. 1.7e-13;
0; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33746 CCACACCTTCCAGGCATTGCCCGCCGCGGATCCAGAGAGC 33786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RR11-67C2"
/clone="The state of the sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,(
Homo sapiens, clone RP11-16P14
Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VECTOR: pBACe3.6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 160654)
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Best Local Similarity
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                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC011879
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of reads

100 bp of 1551 bp in length 100 bp of 1354 bp in length 100 bp of 1143 bp in length

100 bp of 1641 bp in

100 bp

100 bp of 2311 bp in length

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PAT 01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGAACCTGGGGGTCAGGCCCCAGCCGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .13249
/organism="synthetic construct"
/mol type="unassigned DNA"
/db Arref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 20 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.1%; Score 89; DB 2; Length 160654; Best Local Similarity 99.0%; Pred. No. 1.6e-13; Matches 100; Conservative 0; Mismatches 0; Indels 1.
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133059. .145697.
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Sequence 20 from Patent WO0200926
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AX344173.1 GI:18492061
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contig of 2280 bp in length

gap of 100 bp

contig of 668 bp in length

gap of 100 bp

contig of 1770 bp in length

gap of 100 bp

contig of 2682 bp in length

gap of 100 bp

contig of 3028 bp in length

gap of 100 bp

contig of 5028 bp in length

gap of 100 bp

contig of 5028 bp in length

gap of 100 bp

contig of 5133 bp in length

gap of 100 bp

contig of 6130 bp in length

gap of 100 bp

contig of 6130 bp in length

gap of 100 bp

contig of 6130 bp in length

gap of 100 bp

contig of 6130 bp in length

gap of 100 bp

contig of 6140 bp in length

gap of 100 bp

contig of 8161 bp in length

gap of 100 bp

contig of 8622 bp in length

gap of 100 bp

contig of 8161 bp in length

gap of 100 bp

contig of 8161 bp in length

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contig of 8622 bp in length
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of 11557 bp in length
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20624. .22903
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1. 13249
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                         3 AACCTGGGGGTCAGGCCCCCAGCGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCC
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 90 03-JAN-2002;
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Pred. No. 0.00017;
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78.8%; Pred. No. o...
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Seguence 22 from Patent W00202807.
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Sequence 90 from Patent WO0200928.
AX345019
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Location/Qualifiers
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3 AACCTGGGGGTCAGGCCCCCAGCGGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCC
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 19 03-JAN-2002;
Epigenomics AG (DE)
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 89 03-JAN-2002;
Epigenomics AG (DE)
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/db_xref="teaxon:32630"
                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
42.8%; Score 43.2; Di
Best Local Similarity 71.0%; Pred. No. 0.2;
Matches 71; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX345018 13249 bp
Sequence 89 from Patent WO0200928.
                                                                                                                                                                                                                              13249 bp
Sequence 19 from Patent WO0200926.
AX344172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Direct Submission
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACUPEL24 228272 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-134B20, WORKING DRAFT SEQUENCE.
AC098124
                               4159 GGAATTTGGGGGTTTTTAGTCGCGGGAAG-TCGTTTAGGAGCGCGCAAATTTTT 4217
                                                                                                                                                                                                                                                                                                      PAT 06-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4159 GGAATTTGGGGGTTAGGTTTTAGTCGCGGGAAG-TCGTTTAGGAGCGCGCGAAATTTTT 4217
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9
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGAACCTGGGGGTCAGGCCCCAGCCGCGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCT
GGAACCTGGGGGTCAGGCCCCAGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 42.8%; Score 43.2; DB 6; Length 13249; 1 Similarity 71.0%; Pred. No. 0.2; 71; Conservative 0; Mismatches 28; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with cell signalling Patent: WO 0202807-A 21 10-JAN-2002; Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4218 TTATATTTTTAGGTATTTGTTCGTCGCGATTTAGAGAG 4257
                                                                                                                                                            4218 TTATATTTTTTTAGGTATTTGTTCGTCGCGATTTAGAGAG 4257
                                                                                                        61 CCACACCCTTCCAGGCATTGCCCGCCGCGATTCAGAGAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CCACACCCTTCCAGGCATTTGCCCGCGGGATTCAGAGAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC098124.6 GI:30522711
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="synthetic construct"
                                                                                                                                                                                                                                                                                                   AX348563 13249 bp
Sequence 21 from Patent WO0202807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cs AG (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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AC098124/c
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
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VERSION
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SOURCE
                                                                                                                                                                                                                                               RESULT 8
AX348563
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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunzatne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Haves, Y., Hines, S., Haddin, S.L., Hodgson, A., Hogues, M., Hollins, B., Havells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, R., Jackson, L., Jacob, L., Jacob, J., Khan, Z., King, L., Kovar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, M., Liu, Y., Lebow, H., Lovan, J., Lewis, L., Liu, M., Liu, W., Liu, Y., Loulseged, H., Lozado, R.J., Land, S.L., Liu, J., Lourseged, H., Lozado, R.J., Martinez, E., Mangum, A., Mangum, B., Martin, K., Martin, Martin, M., Martin, M., Martin, M., Martin, M., Martin, K., Martin, M., Martin, M., Martin, M., Martin, M., Sarony, G., Scher, K., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Strong, R., Strong, R., Strong, R., Strong, R., Soda, G., Strater, M., Martin, K., Wilson, Y., Wilson, M., Wallson, D., Wallson, D., Wallson, D., Wallson, M., Wallson, M., Wallson, M., Warren, J., Warren, J., Warten, R., Wallson, M., Wallson, M.
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On May 10, 2003 this assembly is a combination of BAC based reads
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.hom.hum.edu/projects/ratf). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
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Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Consensus quality: 212229 bases at least Q40
Consensus quality: 213662 bases at least Q30
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (bases 1 to 228272)
Rat Genome Sequencing Consortium.
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2 (bases 1 to 228272)
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* NOTE: Estimated insert size may differ from sequence length

* See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 228272: contig of 228272 bp in length.
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Rattus norvegicus clone CH230-115H19, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D. Bandaranaike, D. Bazber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Carter, K., Cavaco, I., Cessar, H., Center, A., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
Consensus quality: 214533 bases at least Q20
Estimated insert size: 221650; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAACCTGGGGGTCAGGCCCCAGCCGCGGGAAGCGCCCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7458...8579
/note="wgs end extension
clone end:Sp6"
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/note="wgs_end_extension
clone_end:Sp6"
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/note="wgs_end_extension
clone_end:Sp6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10116"
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lone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (9189.
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Best Local Similarity
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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davisland, L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delagdo, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Durn, A., Durbin, K., Dival, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Franch, C., Enhiely, M., Flaggn, N., Porbes, L., Poster, M., Gebregocygis, B., Ger, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Ganregocygis, B., Ger, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Harnandez, S., Havlak, P., Hamil, C., Hamilton, C., Hamilton, K., Hamilton, K., Hamilton, C., Hamilton, K., Harnandez, N., Havlak, P., Hawes, A., Henderson, M., Hernandez, M., Glorera, M., Gobregocygis, B., Geor, M., Hamil, C., Hamilton, C., Hamilton, K., Harnandez, M., Hawells, S., Hiddun, S. L., Hodgson, A., Hendera, M., Hender, M., Hamilton, K., Mann, C., King, L., Kovar, C., Kowis, C., Kozeft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., London, P., London, M., Malloy, K., Mangum, A., Mansenwari, M., Mahindartne, M., Mahmod, M., Malloy, K., Mangum, P., Martin, R., Martinez, B., Mortin, S., Manicas, E., Mortin, S., Martinez, B., Mortin, M., Mannyer, M., Nair, L., Mannyer, K., Manner, G., Minia, E., Mortin, S., Martinez, B., Mannyer, M., Mannyer, M., Norris, S., Municasa, M., Murchen, E., Paul, H., Perez, M., Perez, L., Peraz, M., Parantak, S., Raid, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Plopper, F., Polideker, A., Perez, M., Perez, M., Perez, M., Perez, M., Perez, M., Band, M., Savery, G., Scherer, S., Scott, G., Stateman, S., Shen, H., Saders, W., Savery, G., Scherer, S., Scott, G., Stateman, S., Sand, H., Sanders, W., Savery, G., Scherer, S., Scott, G., Ranger, M., Savery, G., Scherer, S., Soctle, R., Weille, M., Savery, G., Scherer, S., Soctle, R., Weille, M., Savery, G., Scherer, S., Soctle, R., Weille, M., Weilse, R., We
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Baylor Plaza, Houseron, TX 77030, USA.

The sequence in this sequence version replaced gi:25007772.

The sequence in this assembly is a combination of BAC based reads and whole genome shortgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each consig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Rat Genome Sequencing Consortium.
Direct Submission
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Direct Submission
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Center codê: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine

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TITLE
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                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                       Assembly program: Atlas 3.0;

Consensus quality: 217062 bases at least Q40

Consensus quality: 220975 bases at least Q30

Consensus quality: 223890 bases at least Q20

Estimated insert size: 227972; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 255901: contig of 255801 bp in length
2 255901: gap of unknown length
12 257111: contig of 1210 bp in length
2 257211: gap of unknown length
2 258227: contig of 1016 bp in length.
Location/Qualifiers
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Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-115H19"
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                    Center project name: GKTX
Center clone name: CH230-115H19
------- Summary Statistics
-- Project Information
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/note="wgs_contig"
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AC130592.3 GI:24635281
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Direct Submission.

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 6, 2002 this sequence version replaced gi:23664960.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table bellow represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contigs are ends of the clone and there may be sequence contigs within a contigs and there are may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Drelgado, O., Denson, S., Derman, C., Dutchin, K., Duval, B., Dasav-Rocha, S., Dunn, A., Dutchin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Elgago, V., Porbes, L., Foster, M., Geverra, M., Gebregorgis, E., Geer, K., Gall, R., Garda, A., Garcia, M., Garda, M., Hamilton, K., Hanlandez, M., Hanlas, S., Hadun, W., Hamilton, C., Hamilton, K., Harlandez, M., Hanlas, S., Hadun, S. L., Hongson, A., Hogues, M., Hollins, B., Hawells, S., Hiadun, S. L., Hodgson, A., Hogues, M., Garder, C., Kraft, C. L., Lebow, H., Levan, J., Lidghid, D., Jackson, J., Jackson, L., Jacob, L., Garda, H., Londson, B., Mander, M., Malloy, K., Martin, K., Martin, K., Martin, K., Martin, R., Martin, M., Ma
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Submitted (12-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 307042)
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Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Project Information

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musculus clone rp23-458j13 map 1 strain C57BL/6J, WORKING DRAFT
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3 (bases 1 to 199471)

Li,J., Yang,L. and Roe,B.A.

Direct Submission
Submitted (19-DEC-2003) Department Of Chemistry And Biochemistry,

The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

On Dec 3, 2003 this sequence version replaced gi:38604127.
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Li,J.; Yang,L. and Roe,B.A. Mus musculus BAC Clone rp23-458jl3
                                                                                                                                                                                                                                                                                                                                                          Li,J., Yang,L. and Roe,B.A.
Direct Submission
Submitted (24-AUG-2001) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **NOTE: This is a "working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**Jayos provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**Jayos provided by the submittor.

**Jayos contig of 16368 bp in length 139306 55773; contig of 16800 bp in length 12673; contig of 16800 bp in length 12674 72773; gap of unknown length 159035 179496; contig of 86161 bp in length 159035 179496; contig of 86161 bp in length 179597 188163; gap of unknown length 179597 188163; contig of 8105 bp in length 188264 186268; contig of 8105 bp in length 188264 196368; contig of 8105 bp in length 188264 196368; contig of 8105 bp in length 196369 199471; contig of 3003 bp in length 106471; contig of 3003 bp in length 106471; contig of 3003 bp in length 106469 199471; contig of 3003 bp in length 106469 199471; contig of 3003 bp in length 106469 196468; gap of unknown length 106469 199471; contig of 3003 bp in length 106469 196469; gap of unknown length 106469 199471; contig of 3003 bp in length 106469 199471; contig of 3003 bp in length 106469
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The University of Oklahoma
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/clone_lib="RPCI - 2:
                               SEGUENCE, 8 ordered pieces. AC093452
AC093452.15 GI:38638756
HTG: HTGS PHASE2; HTGS DRAFT.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                               Unpublished
2 (bases 1 to 199471)
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                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* location/Qualifiers
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/note="wgs_end_extension
clone_end:T7"
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[73435, .175226
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complement(6035..6875)
/note="clone_boundary
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169057. .170819
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/note="clone_boundary
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/clone="CH230-506G20"
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/note="clone_boundary
clone_end:Sp6
                       Center project name: KCCD
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Direct Submission
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                                                                                                                                                                                                                           AC093960 253540 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-4G13, WORKING DRAFT SEQUENCE, 3
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                        AC09360.9 GI:30466917
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                        52598 GCCGCGCACCCA 52583
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2 (bases 1 to 253540)
Worley, K.C.
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                  76 CATTTGCCCGCCGCGA 91
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                                                                                                                                                                                                                                                                                   unordered pieces.
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ORGANISM
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KEYWORDS
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Submitted (19-MXY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On May 9, 2003 this sequence version replaced gi:24818990.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.hom.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Submitted (13-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Atlas; Consensus quality: 237398 bases at least Q40 Consensus quality: 237398 bases at least Q30 Consensus quality: 23873 bases at least Q20 Bstimated insert size: 246935; sum-of-contigs estimation Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/db xref="taxon:10116"
/clone="CH230-4G13"
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Center clone name: CH230-4G13
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clone_end:Sp6"_
1060._.3204
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Rat Genome Sequencing Consortium.
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clone_end:Sp6
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                                                                                                                                                                      Direct Submission
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Direct Submission
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256092
256192
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                                                                                                                                                         Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
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1 (Dases I to 257344)

Allan, C. Allan, H. Alshcroks, S., Admin, A., Angudiano, D., Alder, J., Alder, C., Allan, H. Alshcroks, S., Amin, A., Angudiano, D., Alden, C., Allan, H. Alshcroks, S., Amin, A., Angudiano, D., Barden, I., Bardanike, D., Barber, M., Barnstead, M., Bendan, B., Blath, J., Blathenburg, T., Casagar, H., Cener, A., Carter, R., Barry, C., Blath, D., Burrel, K., Calderon, E., Carderas, V., Carter, M., Carter, M., Chen, D., Chen, D., Chen, G., Chacko, J., Charvez, D., Chen, G., Chen, R., Chen, M., Cree, M., D'Gouza, L., Daviala, M., Davis, C., Cockrell, R., Cox, C., Coyle, M., Cree, M., Didya, R., Dagan-Rocha, S., Duun, A., Dutbin, K., Darder, D., Davia, D., Davia, S., Duun, A., Dutbin, R., Dutbin, B., Baves, K., Drand, C., Payer, C., Payer, C., Payer, C., Payer, C., Payer, C., Payer, S., Duun, A., Dutbin, R., Duval, B., Baves, K., Brander, S., Finley, M., Flagg, N., Porbes, L., Forter, M., Gabrier, P., Fraser, C., M., Gabriel, A., Ganta, R., Garcia, A., Garner, T., Garca, M., Gurarandez, S., Finley, M., Flagg, N., Border, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Handerson, N., Hennandez, M., Havlak, P., Hawes, A., Handerson, N., Hennandez, M., Havlak, P., Hawes, A., Handerson, N., Hennandez, M., Maryandez, R., Kelly, S., Khan, Z., King, L., Lay, J., Lay, 
                                                                                                                                                              120760 dedeachrecticherregedendeerregeernageinagestakeerengerengen 120819
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                           9 GGGGTCAGGCCCCAGCCGCGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACCC
                                                     Gaps
                                                     0;
Length 253540;
31.9%; Score 32.2; DB 2; Length 2
59.1%; Pred. No. 1.2e+02;
ive 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCII1855.4 GI:25006939
HTG; HTGS PHASE1; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                       120820 AGCACGACATAAACCCGCTGAGGTACAGCGAGC 120852
                                                                                                                                                                                                                       69 TICCAGGCATITGCCCGCGCGATICAGAGGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                         257344 bp DNR
Rattus norvegicus clone CH230-196H16,
***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 257344)
                                                           55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus.
     Query Match
                                                                                                                                                                                                                                                                                                                                                          RESULT 14
AC111855/c
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                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
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Submitted (19-FEB-2022) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

S Rat Genome Sequencing Consortium.

Direct Submission

Direct Submission

Nov 15, 2002 this sequence Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23270243.

The sequence in this assembly is a combination of BAC based reads and whole genome shotqun sequencing reads assembled using Atlas and whole genome shotqun sequencing reads assembled using Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold in the Sequence ontigs are ordered and oriented, and seguence by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entiraly of whole genome shotqun sequence reads. Both end sequences and whole genome shotqun sequence reads. Both end sequences and whole genome this contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Bstimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: GOJH Center clone name: GOJH Center clone name: CH230-196H16

Assembly program: Phrap; version 0.990329
Consensus quality: 238203 bases at least Q40
Consensus quality: 241708 bases at least Q30
Consensus quality: 244072 bases at least Q20
Estimated insert size: 245085; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 228515; contig of 228515 bp in length 228615; gap of unknown length le 256091; contig of 27476 bp in length 2 256191; gap of unknown length 2 257344; contig of 1153 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CH230-196H16"
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/db_xref="G1:6459089"
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CTVGGGRVPAPYFPRAARRGLSDWGGGFAAAHSSPAQGASALASMYLLLGVWGWTLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGWPEGRAPVAPEGGAPGPFFSDRGGVCWRHPAQVRQGKSGAGP
AGAPLEXTHEFIDTALVDESTREINBWGVLSGYTURBELLVASGRDFFRSTJGETAELV
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LCFSVPQALLAARAGATYVSPFVGRVDDTGWDGSELIRQIKEAFVLGDIQTKVLAASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQVAGEMILAQNEKINWVPGNIKHGRFGNWILEGNVDWAISRERYWGTPLPFWQSESGQL
RYJGSYAELSEBLAGRDLSDLIHRPYTDITFFLDGBEYRWPDBLUDWRPSKGNRYA
QWGLLINGGGEAVRGAEQRAKYPADYICRAIDQTRGWFYSLHAISTWLYDQDRYKNV
ICCAHYDEKGLKOMSSKGNVYAPLPILPDQYGADSVRWYMFWASDPGDQKRFSERLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAQRSYVNTLWNYYSFYU,YANLDQPDIAAAPAYAERPEMDRWLLARLEETVRDYTAA
LESYDARSGGRALEGFYDDLSNWYYRRSRSRFWGEGGTYDTAAYATLHEALLVVSQLT
APFTPFLADALYRNLSGEESSYHLTPWPTVRAERLDRKLTADWAAVMKVYELGRAVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHNLKTRQPLAGVQVRAASPEALDALKRSQTQIMEELNVKAVTFLEGDTDLVQYSLRP
INEVVGKQCYGLPVLKKALTBADARAVATAVORGOGFSVQADGVTFDLTPGSVLVDA
KAPBGVAARBDAGYLVAFDTALTPELVKRGIARDIVRA I QERKKAAGFEVQDRIALAL
ELDGEALEAAQAWQDFIAGEVLAEQVAYGSGEGFRAEVEGGAVTLKKL
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AGTNPVKKBG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLGWLGRNHGASREELEEFNRLCRTSVWETIQDWNELTERMGYWLDLGDPYTTYQNSY
VESVWNLLRRLHEKGLVAQDYKVVPLSPRISSTLSRAELGEVDSYRMVDDPSVYVRLP
IVWDTLPERAHAALSSLSGEQRQGLSLLVWTTTPWTLPSNTLAAVNPDLDYVVADSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRVIVAAEGAVERLSALHKDAAPLEVLARFKGRDLEWVEYEPPFPEVASQLGVVSELHE
RRDGKPVLHFVVWADFVSDVDGSGVAHEAPAYGAEDLEVARAYGVPLMFGVDDHGILQ
VTHEQGKFFKDADKGLIADWKARGLMFWAGTLKHRYPFHDRTGDPILYFAKKGWYIRT
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                                                                                                                                                                        'note="similar to GB:X75439 GB:X59478 SP:P41368 PID:581558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:M76990 SP:P07775 PID:141751 percentidentity: 59.18; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6341. .7201
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                                                                                                                                                                                          percent identity: 59.12; identified by sequence similarity; putative" /codon start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identified by sequence similarity; putative"
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/transl_table=11
/product="transport protein, putative"
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                                                                                                                  complement (1432. .4668)
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                                                               complement (1432. .4668)
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FHRKSGQHTAHLGSFWNGCAARTERGIEQSCCALIDVQHRQAFTVDVRQTRTGSEAPS
RLEQAADQLDDVLLDLQTVPRLDLAAVVADGNYAKESMVETVTGHGLPFISRFPRNAN
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VVI QQVGKKGQVTGYAVLFSTAVTMPAHEVIALYRSRFEIELI FRDAKQFLGGQDVQL
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1 (bases 1 to 12557)

White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haff,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Noffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Wamathevan,J.J., Lam,P., MoDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et al. Genome sequence of the radioresistant bacterium Deinococcus radiocacus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., White, O., Eisen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., Modson, K.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Moffet, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, M., Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Wakarovan, K.S., Aravind, L., Daly, M.J., Minton, K.W., Saravind, L., Daly, M.J., Minton, K.W., Smith, H.D., Ketchum, K.A., Nelson, K.E., Salzberg, S., Smith, H.O., Venter, J.C. and Fraser, C.M.
Direct Submission
Submitsed (08-NOV-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                              9 GGGGTCAGGCCCCAGCCGCGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACCC
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE001980 12557 bp DNA linear BCT 22-NOV
Deinococcus radiodurans R1 section 117 of 229 of the complete
                                                                  Length 257344;
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                                                                                                                        38; Indels
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                                                                                                                                                                                                                                                                                                                                                         174739 AGCACGACATAAACCCGCTGAGGTACAGCGAGC 174707
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Pred. No. 1.2e+02;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                      69 TICCAGGCATITGCCCGCCGCGATICAGAGAGC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:243230"
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/gene="DR1334"
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Deinococcus radiodurans R1
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AE001980.1 GI:6459086
                                                                     31.9%;
59.1%;
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DLSALAANLPAGIAFGGQDVSAHESGAYTGELSAAMIKDAGASCVVVGHSERREYHDE
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EPVWAIGTRYTALDDAEELAAIRGALREQYGARAEGIRVLYGGSVKPENIAEICGK
PNVNGALVGGASLLKPDVLGMLDALR"
COMPLEMENT (9416. .9778)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(9116. .9778)
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complement (8620. .9354)
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db_xref="G1:6459096"
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complement (9775. .10209)
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'transT_table=11
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31.7%; Score 32; DB 1; Length 12557;

Query Match

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                                                   1 GGAACCTGGGGGTCAGGCCCCAGGCGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCT
                   Gaps
                   0;
                   40; Indels
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                                                                                                                       61 CCACACCCTTCCAGGCATTTGCCCGCCGCGATTCAG 96
   Pred. No. 1.7e+02;
0; Mismatches 40
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     58.3%;
                        56; Conservative
Best Local Similarity
Matches 56; Conserv
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AAS69625 nm38g05.s BE42248 CM1-HT014 CE268863 tigar-gss-A0373217 RPCIII-14 BX480547 DXFZp686C

CF181752 818731 MA

BI057063 PM2-GN050

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Run on:

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L. Unpublished (2003)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the bovine BAC library CHORI-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXECUTE 195824.TVB CHORI-240 Bos taurus genomic clone CH240_195824, genomic survey sequence.
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                                                                                BIO57063
AU12290
AQ27080
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AQ373217
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Bos taurus (cow)
Bos taurus
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VERSION
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SOURCE
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CF362037 828421 MA
CE678956 tigr-gss-
CF364190 834119 MA
                                                                                               7, 2004, 13:34:53 ; Search time 1484.07 Seconds (without alignments) 1629.864 Million cell updates/sec
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                                                                                                                                                                                                                                                                                  55026578
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                   27513289 segs, 14931090276 residues
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                                                                                                                                                       US-10-071-411A-1_COPY_500_580
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Maximum Match 99%
Listing first 45 summaries
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CF362037
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Gapop 10.0 , Gapext 1.0
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Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                 165 AAGAAAGTGAGAAGACAACCCACAGAATGAGAAAAATATTTGCCAATCACATATCTGAT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis. [ bases 1 to 652)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Verter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CE678956
tigr-gas-dog-17000313980922 Dog Library Canis familiaris genomic,
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                         /note="Vector: pcDNA3.1; Site 1: EcoR1; Site 2: Not1; Library made with RNA pooled from multiple tissues including brain, liver, muscle, placenta/endometrium, ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                    3 AAGAAAGTGAAAACACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT
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/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="standard Poodle"
/db_xref="taxon:9615"
/clone_lib="hog Library"
/note="Site 1: BetX1; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                    Query Match
60.0%; Score 48.6; DB 14; Length 603;
Best Local Similarity 75.9%; Pred. No. 0.0022;
Matches 60; Conservative 0; Mismatches 19; Indels 0
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75.9%; Pred. No. 0.0022;
iive 0; Mismatches 19;
     'clone lib="MARC 3PIG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
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Canis familiaris
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Best Local Similarity
Matches 60; Conserv
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1 (Dases 1 to 603)

S mith, T.P. L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J.,
Wise, T.A., Nonneman, D.J., Wray, J.E. and Reele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized library

L Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: SRGB018 cow: J column: 16
Seq primer: GTAATACGACTCACTATAGGG.
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(http://www.chori.org/bacpac/bovine240.htm). For BAC library wavallability, please contact Pieter de Jong (pdejong@mail.cho.org) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Blood"
/clone_lib="CHGRI-240"
/note="Vector: PTARBACL:3; Site_1: MboI; Site_2: MboI;
Hereford bull ill Domino 99375; CHGRI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.6; DB 28; Length 832;
Pred. No. 0.00061;
0; Mismatches 19; Indels 0
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828421 MARC 3PIG Sus scrofa CDNA 5', mRNA sequence.
CF362037
                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
/clone="CH240_195F24"
                                                                                                                                                                    Plate: 195 row: F column: 24 Seg primer: T7 Class: BAC ends.
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1 Similarity 76.5%;
62; Conservative (
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Sus scrofa
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Best Local S
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NG-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image-html
Insert Length: 339 Srd Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4366 Fax: 402 762 4360 Enail: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: SRG8013 row: J column: 7 Seq primer: GTAATACGACTCACTATAGGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /issue_type="pooled"
//lab host="mailth"
//lab host="halt0"
//lab host
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1. .701
/organism="Sus scrofa"
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/db_xref="taxon:9606"
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/db_xref="taxon:9823"
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Homo sapiens
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Unpublished (1997)
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Contact: Smith TPL
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
FO Box 166, Clay Center, NE 68933-0166, USA
Fal: 402 762 4366
Fax: 402 762 4390
Fmail: SmithOemail.marc.usda.gov
Final: SmithOemail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
Coross match.v0.990329.
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.U., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized
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/db xref="taxon:9823"
/tishue_type="pooled"
/lab host="DH108"
/clone_lib="WARC 3PIG"
/note="Vector: pcDNA3.1, Site 1: BcoRI; Site 2: NotI;
/note="vector: pcDNA3.1, site 2: NotI; site 3: NotI;
/note="vector: pcDNA3.1, site 3: NotI; si
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1 (Dases I to 701)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J.,
Wise, T.A., Nonnean, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized
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                                                                    CF364190 657 bp mRNA linear
834119 MARC 3PIG Sus scrofa cDNA 5', mRNA sequence.
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USDA, ARS, US Meat Animal Research Center
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

Finis sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-HT0141-170 999-013-h05&t3=1999-09-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
High quality sequence stop: 361.
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1 (bases 1 to 361)

1 (bases 1 to 361)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., Corras, C., Asimpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
/clone_lib="NCI_CGAP_Pr4.1"
/clone_lib="NCI_CGAP_Pr4.1"
/note="Organ: prostate; Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (high-grade), cDNA made by oligo-dr priming. Non-directionally cloned.
Size-selected on agarcae gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE142248 361 bp mRNA linear EST 21-JUN-2000 CM1-HT0141-170999-013-h05 HT0141 Homo sapiens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/db_stege="Adult"
/clone lib="HT014"
/note="Organ: head_neck; Vector: pucl8; Site_1: SmaI;
                                                                                                                                                                                                                                                                                                                                                          1 TCAAGAAAGTGAAAACACAAAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
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                                                                                                                                                                                                                                                                     Score 47.4; DB 9; Length 360;
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Site 2: Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
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The Institute for Genomic Research
Department of Eukarycnic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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(Dases 1 to 422)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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                                                                                                                                                                                                                                                                                                          81 roaagaaargaaagacaaccoragcagaacagaaararrircacaraardrarcig 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligr-gss-dog-17000359927985 Dog Library Canis familiaris genomic, genomic, survey sequence.
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/clone lib="bog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                 Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 47.4; DB 29; Length 74.1%; Pred. No. 0.0049; Live 0; Mismatches 21; Indels
                                                                                                                                                                                                                         Indels
                                                                                                                                                                               58.5%; Score 47.4; DB 10; 74.1%; Pred. No. 0.005; ive 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Canis familiaris"
                                                                                                              low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Canis familiaris
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Best Local S
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Tel: +55-11-2704922
Fax: +55-11-2707001
(bases 1 to 657)
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Best Local Similarity
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REFERENCE
                               AUTHORS
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                            RPCT11-146MZ0.TV RPCI-11 Homo sapiens genomic clone RPCI-11-146MZ0, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hbe@rigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: I?
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 643)
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/clone lib="RPOI-11"
/note="Vector: pBACe3.6; Site_1: BcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. Venter,J.C.
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/clone="RPCI-11-146M20"
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/db_xref="GDB:7555987"
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BX480547.1 GI:31917361
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AQ373217.1 GI:4344240
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                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Conservative
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BX480547/c
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      RESULT 9
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 583)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coste,F.F., Coldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI057063 585 bp mRNA linear EST 15-JUN-2001
PM2-GN0500-220201-002-h01 GN0500 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hlcc3)"
Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKZ); Email s.wiemann@dKz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp686C23222) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin. Charlottenburg, GRRWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAAATGTCTGTAAGTCATGTATCCG
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Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
Contact: MIPS
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Pred. No. 0.0046;
0; Mismatches 21;
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/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
/clone="DKFZp686C23222"
/dev_stage="adult"
/lab_host="DH108"
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AU122280 Test 01-AUG-2002 AU122280 MAMMAI Homo sapiens cDNA clone MAMMAI002056 5', mRNA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 752)
                                                                                                                                 /close lib="Groots" | Vector: puc18; Site 1: |
/note="Organ: placenta normal; Vector: puc18; Site 1: |
/note="Organ: placenta normal; Vector: puc18; Site 1: |
Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 13 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Enail: genomicsehri.co.jp
Enail: genomicsehri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 CAAGAAAGCAGAGAGACAAACCCACAGAATGGCAGAAAATATTTGTAAATCATGTATCCGA
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.3%; Score 47.2; DB 12; Best Local Similarity 76.3%; Pred. No. 0.0053; Matches 58; Conservative 0; Mismatches 18;
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/clone_lib="MAMMA1"
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                                              'organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
ocation/Qualifiers
                                                                                                                     'dev stage="Adult"
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Contact: Takao Isogai
Genomics Laboratory
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Homo sapiens
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1 (bases 1 to 625)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., de Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-GN0500-
220201-002-b06&t3=2001-02-22&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI057060 625 bp mRNA linear EST 15-JUN-2001
PM2-GN0500-220201-002-b06 GN0500 Homo sapiens cDNA, mRNA sequence.
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  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-GN0500-
220201-002-h01&t3=2001-02-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 523.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 0.0053;
0; Mismatches 18; Indels 0
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58; Conservative
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462 bp DNA linear GSS 03-NOV-1998
HS_2059_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2059 Col=14 Row=A, genomic survey
                          21 TCAGGANAATGAAAAGACACCCCACAGAATGGGAAAAATTTTGTAAATCATATATCCG 80
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  62
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
    3 AAGAAAGTGAAAACACACCCCCCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington Assaington 99109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:966"
|clone="plate=2059 Col=14 Row=A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2059 row: A column: 14
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 462.
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                                                                                                                  680 AAGGGTCTAGTATCCAGAA 698
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                                                                              63 TAGAGACTICIAICCAGGA
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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VERSION
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PUBMED
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                            AQ270907
LOCUS
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Unpublished (1997)

Char GSSs: RPCIII-141MI.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Bukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0200

Email: bhe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search/bac_end_search.html

Seg primer: SP6

Class: BAC ends.
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1 (bases 1 to 569)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
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RPCII1 Human Male BAC Library"
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1 Similarity 73.8%; Pred. No. 0.0088;
59; Conservative 0; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7, 2004, 15:42:30
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7, 2004, 14:31:30 ; Search time 167.215 Seconds (without alignments) 2194.362 Million cell updates/sec
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1 tcaagaaagtgaaaacacaa......ttagagacttctatccagga
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2941586 segs, 2264995651 residues
                                                                                                                                                                                                                                                                                                                                                                                                US-10-071-411A-1_COPY_500_580
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Maximum Match 99%
Listing first 45 summaries
                                                                                                                                                        OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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		ф			SUMMARIES		
Result No.	Score		Query Match Length DB	DB	ID	Description	
1	60.4	74.6	13249	15	US-10-311-455-90	Sequence 90, Appl	
. 1	2 58.6	72.3	13249	15	US-10-311-455-89	Sequence 89, Appl	
ט	3 51	63.0	331	13	US-10-085-783A-12549	Sequence 12549, A	
ű	1 51	63.0	331	16	US-10-242-535A-12549	Sequence 12549, A	
v	5 50.2	62.0	72332	12	US-10-052-482-58	Sequence 58, Appl	
•	5 49	60.5	95683	13	US-10-087-192-160	Sequence 160, App	
o	7 47.4	58.5	592	13	US-10-027-632-48192	Sequence 48192, A	
υ	3 47.4		592	13	US-10-027-632-48193	Sequence 48193, A	
U	47.4	58.5	592	13	US-10-027-632-48194	Sequence 48194, A	
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υ υ	47.4		592	16	US-10-027-632-48193	Seguence 48193, A	
0	3 47.4	58.5	592	16	US-10-027-632-48194	Sequence 48194, A	
٦ ن	47.4	58.5	592	16	US-10-027-632-48195	Sequence 48195, A	

61 ATTAGAGACTICTAICCA 78

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78918,	Sequence /8919, A Sequence 78920, A	78921,	Sequence 314671,		Seguence 314673,		Sequence 78918, A			Sequence 78921, A	Sequence 314671,			Sequence 314674,		187,		Sequence 76212, A	Sequence 76212, A	Sequence 146, App	Sequence 41212, A	Sequence 41212, A	Sequence 202, App	Sequence 18323, A	Sequence 199, App	Sequence 196, App	e 18518,	Sequence 6173, Ap	12451,
3 US-10-027-632-78918	3 US-10-02/-632-/8919 3 US-10-027-632-78920	3 US-10-027-632-78921	3 US-10-027-632-314671	3 US-10-027-632-314672	3 US-10-027-632-314673	3 US-10-027-632-314674	6 US-10-027-632-78918	6 US-10-027-632-78919	US-1	6 US-10-027-632-78921		6 US-10-027-632-314672			3 US-10-282-174-186	3 US-10-282-174-187	3 US-10-282-174-484	13 US-10-027-632-76212	16 US-10-027-632-76212	US-09-920-455-146	13 US-10-085-783A-41212	16 US-10-242-535A-41212	US-09-920-455-202	10 US-09-814-353-18323	US-09-920-455-199	US-09-920-455-196	US-09-814-353-	10 US-09-814-353-6173	0 US-09-814-353-12451
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47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	45.8	45.8	45.8	45.8	45.8	45.8	45.8	45.8		45.8
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ALIGNMENTS

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RESULT.

US-10-311-455-90/C

Sequence 90, Application US/10311455

Publication No. US20030143606A1

Sequence 90, Application US/10311455

Publication No. US20030143606A1

SEGUENCAL INFORMATION:

APPLICANT: PIEPENBRCKK, Christian

FILE REPERENCE: 5013-1014

CURRENT FILING DATE: 2001-07-07

PRIOR PELING DATE: 2001-07-07

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01

PRIO
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Sequence 12549, Application US/10242535A

Publication No. US20040013663A1

GENUREL INFORMATION:
APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
TITLE OF INVENTION: Compositions and Methods Relatining to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A

FILE REFERENCE: 2002-09-12
FRIOR APPLICATION NUMBER: US 10/085,783
FRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-02-28
FRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

FRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE PATENTING DATE: 2010-02-28

NUMBER OF SEQ ID NOS: 58994

SEQ ID NO 12549
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APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
APPLICANT: Morris, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PLLING DATE: 2000-12-22
PRIOR PLLING DATE: 2001-03-02
                                        Length 331;
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                                    63.0%; Score 51; DB 13; Length 33 78.9%; Pred. No. 2.8e-07; ive 0; Mismatches 16; Indels
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; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-12549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 58, Application US/10052482; Publication No. US20040072264A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 TAAGGGACTIGTATCC 77
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Best Local Similarity 78.93
Matches 60; Conservative
                                        Query Match
Best Local Similarity 78.9
Matches 60; Conservative
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ORGANISM: Human
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US-10-052-482-58/C
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| Sequence 89, Application US/10311455 |
| Sequence 89, Application US/10311455 |
| Sequence 89, Application US/10311456 |
| Sequence 89, Application OS-01030143606A1 |
| Sequence 89, Application No. US20030143606A1 |
| SEDENEAL INFORMATION: PIERDAMPOCK, Christian APPLICANT: PIERDAMPOCK, Christian APPLICANT: BEBLIN, Kurt |
| TILLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern |
| TILLE OF INVENTION: Cytosine methylation |
| FILE REFERENCE: 5013.1014 |
| CURRENT APPLICATION NUMBER: DE 10032529.7 |
| PRIOR APPLICATION NUMBER: DE 10043826.1 |
| PRIOR APPLICATION NUMBER: DE 10043826.1 |
| PRIOR FILING DATE: 2000-09-01 |
| NUMBER OF SEQ ID NOS: 2424 |
| LENGTH: 13249 |
| MANDER OF SEQ ID NOS: 2424 |
| LENGTH: NUMBER OF SEQ ID NOS: 2424 |
| MANDER 
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| Publication No. US20040037841A1 |
| GENERAL INFORMATION: |
| APPLICANT: Chondrodene Inc. |
| APPLICANT: Chondrodene Inc. |
| APPLICANT: Chondrodene Inc. |
| APPLICANT: Liew, C.C. |
| TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis |
| FILE REFERENCE: 221/2002 |
| CURRENT APPLICATION NUMBER: US/10/085,783A |
| CURRENT FILING DATE: 2002-02-28 |
| PRIOR APPLICATION NUMBER: US 60/275,017 |
| PRIOR FILING DATE: 2001-03-12 |
| PRIOR FILING DATE: 2001-03-12 |
| PRIOR FILING DATE: 2001-03-28 |
| NUMBER OF SEQ ID NOS: 58994 |
| SOFFWARE: PREAUTIN Version 3.2 |
| CONTRACTION NOTES |
| CONTRACTION NUMBER: 2001-02-28 |
| NUMBER OF SEQ ID NOS: 58994 |
| CONTRACTION NOTES |
| PRIOR APPLICATION NUMBER: US 60/271,955 |
| PRIOR FILING DATE: 2001-03-28 |
| NUMBER OF SEQ ID NOS: 58994 |
| CONTRACTION NOTES |
| CONTRACTI
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Pred. No. 2.7e-09;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-89
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) LOCATION: (137)...(137)

; CTHER INFORMATION: n is a, c, g, or

US-10-085-783A-12549
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ch 72.3%;
1 Similarity 82.7%;
67; Conservative (
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 67; Conserv
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LENGTH: 331
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341 TCAAAAAAGTGAAAATACAACCAACAGAAAGAGAAAAAATATTTTCAAACCATGTATCTG 282
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PELICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FBALESQ for Windows Version 4.0
SEQ ID NO 48193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCAAGAAAGTGAAAAACACCAGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.5%; Score 47.4; DB 13; Length 74.1%; Pred. No. 5.6e-06; cive 0; Mismatches 21; Indels
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                                                  FRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR PILING DATE: 1999-09-38
                                  FILING DATE: 2000-07-12
APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48193, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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Best Local Similarity 74.1
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human
US-10-027-632-48192
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ORGANISM: Human
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827 128
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                         NAME/KEY: misc feature

LOCATION: (70768)..(71491)

CTHER INFORMATION: "n" at positions 70768 to 71491 can be any base

US-10-052-4812-58
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0
                                                                                                                                                                                                                                                                                                                                                            62.0%; Score 50.2; DB 12; Length 72332; 77.2%; Pred. No. 3.3e-06; ive 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 95683;
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| Publication No. US20020182586A1
| SEMERAL INFORMATION:
| APPLICANT: Morella David W.
| APPLICANT: Morella David W.
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CURRENT APPLICATION NUMBER: US/10/087,192
| CURRENT APPLICATION NUMBER: US/20/087,192
| CURRENT APPLICATION NUMBER: US/20/147,377
| PRIOR FILING DATE: 2000-12-22
| PRIOR FILING DATE: 2001-03-02
| PRIOR FILING DATE: 2001-03-02
| NUMBER OF SEQ ID NOS: 2059
| SOFTWARE: FastSEQ for Windows Version 4.0
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NUMBER OF SEQ ID NOS: 241
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
LENGTH: 72332
                                                                                                                                                                                                                                                                                                                                                                                                                           61; Conservative
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US-10-087-192-160
                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
Matches 61; Conserva
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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US-10-027-632-48192/c
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LENGTH: 95683
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US-10-087-192-160
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341 TCAAAAAAGTGAAAATRCAACCAACAAGAGAAAAAAAAATATTTCAAACCATGTATCTG 282
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WEDILCACTACION NO. US20020198371A1

SEQUENCE 48194, Application US/10027632

SEQUENCE 108202 0.082020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

FRIOR APPLICATION NUMBER: US 60/128,006

PRIOR APPLICATION NUMBER: US 60/199,676

PRIOR APPLICATION NUMBER: US 60/199,676

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 1999-10-09

PRIOR FILING DATE: 1999-06-09

PRIOR FILING DATE: 1999-06-09
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE REFERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04.30
PRIOR APPLICATION NUMBER: US 60/128,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
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Best Local Similarity
Matches 60; Conserv
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US-10-027-632-48195/c
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US-10-027-632-48194
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341 TCAAAAAGTGAAAATTACAACCAACAAGAGAAAAAAAAATATTTTCAAACCATGTATCTG 282
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Bequence 48192, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

PRIOR REPLICATION NUMBER: US 60/198,006

PRIOR PELING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-24

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-08-08

PRIOR PLING DATE: 1999-08-08

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-08

PRIOR PLING DATE: 1998-08-08

PRIOR PLING DATE: 1998-08-08

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ilarity 74.1%; Pred. No. 5.6e-06;
Conservative 0; Mismatches 21;
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR PRILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41195
LENGTH: 592
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Matches 60; Conserv
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US-10-027-632-48195
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281 ATAAGGGTCTAGTATCCAGAA 261
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Best Local Similarity
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US-10-027-632-48195
                                                                                          ; ORGANISM: Human
US-10-027-632-48194
SEQ ID NO 48194
LENGTH: 592
                                                               TYPE: DNA
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                                 Sequence 48193, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-24

PRIOR PRILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR PRILING DATE: 1999-108-28

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09
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Publication No. US20030204075A9
Publication No. US20030204075A9
Fublication No. US20030204075A9
Fublication No. US20030204075A9
Fublication No. US20030204075A9
Fublication No. US2003020406
Fublication No. US2003020406
Fulls Reference: 108027.129
CURRENT APPLICATION: POLYMORPHS: US/10/027,632
CURRENT PILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-08-09
FRIOR FILING DATE: 1999-09-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
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FRIOR FILING DATE: 1999-08-09
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Matches 60; Conservative
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US-10-027-632-48194/c
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ORGANISM: Human
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Publication No. US20030204075A9
FUBLICATION No. US20030204075A9
GENERAL INFORMATION:
APPLICAMY: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-08
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR FILING DATE: 1999-08-09
FRIOR FILING DATE: 1999
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Sequence 78918, Application US/10027632

Publication No. US2020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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          Length 592;
                                                                                                               Indels
Score 47.4; DB 16;
Pred. No. 5.6e-06;
0; Mismatches 21;
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Search completed: May 7, 2004, 17:35:53 Job time: 170.215 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

7, 2004, 13:35:03 ; Search time 40.6738 Seconds (without alignments) 1105.159 Million cell updates/sec Run on:

1 tcaagaaagtgaaaacacaa......ttagagacttctatccagga 81 US-10-071-411A-1_COPY_500_580 Perfect score: Sequence: Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 segs, 277475446 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

Issued Patents NA:*

/ GgDZ_6/ptodata/2/ina/5A_COMB.seq:*
/ CgDZ_6/ptodata/2/ina/5B_COMB.seq:*
/ CgDZ_6/ptodata/2/ina/6A_COMB.seq:*
/ CgDZ_6/ptodata/2/ina/6B_COMB.seq:*
/ CgDZ_6/ptodata/2/ina/6B_COMB.seq:*
/ CgDZ_6/ptodata/2/ina/PcTUS_COMB.seq:*
/ CgDZ_6/ptodata/2/ina/PcTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB

Sequence 59, Sequence 59, Sequence 59, Sequence 59, Sequence 59, Sequence 59, Description Sequence Sequence 1 Sequence Sequence Sequence Sequence Sequence 3 Sequence 3 Sequence Sequence 3 Sequence Sequence Sequence Sequence Sequence US-09-123-912-59 US-09-643-597-59 US-09-80-642-59 US-09-506-421B-59 US-09-221-107-59 US-09-221-107-59 US-09-426-290-1 US-09-873-404-3 US-09-873-404-3 US-09-873-404-3 US-09-873-1330-211 US-09-873-1330-211 US-09-621-976-1442 US-09-621-976-149 US-09-621-976-189 39.3 392000 39.0 31208 39.0 98844 39.0 116592 38.8 343 4080 38564 392000 10607 168575 63588 3001 99916 786431 41.7 40.7 40.7 40.7 31.8 31.8 31.6 31.6 31.6 0 0 0 0 0 0 0

59, Appl 59, Appl 59, Appl 59, Appl 59, Appl 1342, Appl 1, Appli 3, Appli 27, Appli

									Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
US-09-062-451-72	US-09-289-198-72	US-09-429-755-72	US-09-783-203-1	US-09-733-294A-30	US-09-818-512-3	US-09-497-855A-37	US-09-497-855A-44	US-10-204-708-61	US-09-621-976-1855	US-09-621-976-1849	US-09-734-674-3	US-09-461-325-102	US-10-012-542-102	US-09-784-316-3	US-08-991-789A-191	US-09-062-451-191
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88.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.5	38.3	38.3	37.3	37.0	37.0	37.0	36.8	36.8
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2.8	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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US-09-040-984-59/c
; Sequence 59, Application US/09040984
; Patent No. 6210883
; PATENT No. 6210883
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, TongTong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS;
; TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAAL, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELEDOMUNICATION INFORMATION:
TELEDENONE: 200-622.4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 206-282-6031
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US-09-040-984-59
                                                                                                                                                                                                                                                                                                                        STATE:
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Gaps ; 0 Length 649; Indels Query Match
Best Local Similarity 72.8%; Pred. No. 1.6e-06;
Matches 59; Conservative 0; Mismatches 22;

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Sequence 3 Sequence 7

US-08-991-789A-72

Sequence

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TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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APPLICANT:
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                                                                                                               Sequence 59, Application US/09123912A

Sequence 59, Application US/09123912A

Patent No. 6312695

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER

FILE REPERENCE: 2101213.455C1

CURRENT APPLICATION NUMBER: US/09/123,912A

PRIOR PRING APPLICATION NUMBER: 09/040,802

PRIOR FILING DATE: 1998-03-18

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patentin Ver. 2.0

LENGTH: 649
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COTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-59
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                                  249 Arakiggicragaariccagaa 229
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LOCATION: (22)
OTHER INFORMATION: Where n is a, C,
NAME/KEY: modified_base
LOCATION: (190)
OTHER INFORMATION: Where n is a, C,
NAME/KEY: modified_base
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OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
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OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
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OTHER INFORMATION: Where n is a,
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61 ATTAGAGACTTCTATCCAGGA
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OTHER INFORMATION: Where n is NAME/KEY: modified_base
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OTHER INFORMATION: Where n is NAME/KEY: modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                        RESULT 2
US-09-123-912-59/c
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                          APPLICANT: Eanger, Garry R.
APPLICANT: In, Samuel X.
APPLICANT: Hanger, Agin
APPLICANT: Mang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Morell, Patricia D.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENDE: 210121.455011
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
IBNGTH: 649
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APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nanchael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DAFF: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH : 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-480-884A-59/c

'Sequence 59, Application US/09480884A

'Patent No. 6482591

; GENERAL INFORMATION:
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US-09-643-597-59/c
; Sequence 59, Application US/09643597
; Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATTAGAGACTICTATCCAGGA 81
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REACURE:

REATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(649)

COTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                 Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 72.8
Matches 59; Conservative
                                                                            GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
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Gaps

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1 TCAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
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APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REPERENCE: 210121.455.2
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 649
                                                                                                                                                                                                                                              56.5%; Score 45.8; DB 4; Length 649; 72.8%; Pred. No. 1.6e-06; Live 0; Mismatches 22; Indels
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 649
TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                           61 ATTAGAGACTTCTATCCAGGA 81
                                                                                                                                          NAME/KEY: misc_feature

CCATION: (1)...(649)

OTHER INFORMATION: n = A,T,C or G

US-09-606-421B-59
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OTHER INFORMATION: Where n is a, FEATURE:
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NAME/WES:
LOCATION: (433)
OTHER INFORMATION: Where n is
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OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                      59; Conservative
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LOCATION: (190)
OTHER INFORMATION: Where
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OTHER INFORMATION: Where
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OTHER INFORMATION: Where
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NAME/KEY: modified base
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                                                                                                                                                                                                                                                               Best Local Similarity
Matches 59; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                           FEATURE:
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  Query Match 56.5%; Score 45.8; DB 4; Length 649; Best Local Similarity 72.8%; Pred. No. 1.6e-06; Matches 59; Conservative 0; Mismatches 22; Indels
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APPLICANT: Skelky, Zasir A.W.
APPLICANT: Skelky, Zasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILLING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Banger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERBUCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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US-09-606-421B-59/c
; Sequence 59, Application US/09606421B
; Patent No. 65431315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                      US-09-542-615A-59/c
; Sequence 59, Application US/09542615A
; Patent No. 6518256
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; LOCATION: (1)...(649)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-59

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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Best Local Similarity 72.8%
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Fan, Liqun
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ORGANISM: Homo sapien
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APPLICANT: Wang, T
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LENGTH: 649
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APPLICANT:
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12256 TCAAGAGTATGAAAAGGAAAACCTACAAAATAGGAGAACATGTTTGGAAATCATGTATTTG 12315
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Patent No. 6500656
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
PILE REFERENCE: CL001212-CIP
                                                                                                                                                                                                                                                    1 TCAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60
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                                                               52.6%; Score 42.6; DB 4; Length 4080; 70.4%; Pred. No. 2.9e-05; ive 0; Mismatches 24; Indels 0
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'0.011;
rhes 28; Indels
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APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 168575
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; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
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                                               Query Match
Best Local Similarity 70.49
Matches 57; Conservative
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ORGANISM: Homo Sapiens
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Best Local Similarity
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      US-09-016-434-1342
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US-09-426-290-1
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NAME/KEY:
LOCATION:
NAME/KEY:
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| Patent No. 6500938
| GENERAL INFORMATION:
| APPLICANT: Janice Au-Young
| APPLICANT: Jeffrey J. Seilhamer
| TITLE OF INVENTION: PATHWAY GENE EXPRESSION
| TITLE OF INVENTION: PATHWAY GENE EXPRESSION
| NUMBER OF SEQUENCES: 1490
| CORRESPONDENCE ADDRESS: 1490
| CORRESPONDENCE ADDRESS: 1400
| STREET: 31174 PORTER DRIVE
| STREET: ALL ALLO FORTER DRIVE
| CITY: PALO ALTO
| STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 649;
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MEDIUM TYPE: FOPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: FOPPY disk
COMPUTER: BM PC COMPATIBLE
COREMATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: World Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE: FORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: ZEALLEY, KALEN J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,07
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45.8; DB 4;
Pred. No. 1.6e-06;
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FEATURE:
NAME/KEY: modified_base
LOCATION: (577)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                       COTHER INFORMATION: Where n is a, US-09-221-107-59
                                                                                                                                              NAME/KEY: modified_base
LOCATION: (583)
OTHER INFORMATION: Where n is a,
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1 Similarity 72.8%;
59; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                             NAME/KEY: modified base
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Best Local Similarity
Matches 59; Conserva
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US-09-016-434-1342
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55300 TCAACAGAGTAAATAGACAACCTACAGAATAGAAGAAAATATTTGCAAACTATGCATCCA
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1 Similarity 67.6%; Pred. No. 0.0045;
50; Conservative 0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE KEFERENCE: FZOLDFIL

CURRENT PELICATION NUMBER: US/09/288,143

CURRENT FILING DATE: 1999-04-08

EARLIER APPLICATION NUMBER: PCT/US99/21142

EARLIER PILING DATE: 1999-10-08

EARLIER PELING DATE: 1997-10-09

EARLIER PELICATION NUMBER: 60/061,529

EARLIER PELING DATE: 1997-10-09

EARLIER FILING DATE: 1997-10-09

EARLIER PELING DATE: 1997-10-09

NUMBER OF SEQ ID NOS: 219

COFTWARE: PATENTN VAT: 2.0

SOFTWARE: PATENTN VAT: 2.0
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 4
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 65588
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55240 ACAAAGGICTAATATCCAG 55222
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'Sequence 27, Application US/09288143
'Patent No. 6433139
'GENERAL INFORMATION:
                                                                                                                                                                                                                              NAME/KEY: misc_feature; LCATION: (1)...(63588)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity
Matches 50; Conserva
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1 TCAAGAAAGTGAAAACACAAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60

RESULT 12 US-09-539-333D-211

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TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-621-976-1442
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Patent No. 6630334

GENERAL INPORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001067

CURRENT APPLICATION NUMBER: US/09/751,389

CURRENT APPLICATION NUMBER: 2001-01-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASISEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 786431
                                                                                                                                                                                                                                                           APPLICANT: GAN, Weiniu

APPLICANT: GAN, Weiniu

TITLE OF INVENTION: 1SOLATED HUMAN ENZYME PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOL147

CURRENT APPLICATION NUMBER: US/09/816,095

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 5

SOFTWARR: FASTESEQ for Windows Version 4.0

SEQ ID NO S: 5

LENGTH: 99916
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1313 TGAGCAAAGTAAGCAGACAACCCACAGAGTGAGAAAAAATATTTGCAAACTATGTATCTG 1372
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42.7%; Score 34.6; DB 4; Length 786431;
Best Local Similarity 64.2%; Pred. No. 0.053;
Matches 52; Conservative 0; Mismatches 29; Indels 0;
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Pred. No. 0.032;
0; Mismatches 29; Indels 0;
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COTHER INFORMATION: n = A,T,C or G
US-09-751-389-3
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// LCCATION: (1)...(99916)

// OTHER INPORMATION: n = A,T,C or G

US-09-816-095-3
                                                                                              1373 ACAAAGGACTAATATCCA 1390
                                                                                                                                                                                                                     Sequence 3, Application US/09816095 Patent No. 6664084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 64.2%;
Matches 52; Conservative
                                                  ATTAGAGACTTCTATCCA
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ORGANISM: Human
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US-09-751-389-3/C
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US-09-816-095-3
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367146 TCAACAAAGTGAATAGACAACCCACTGAATGGGAGAAAATATTTGCAAACTACCTATCTG 367087
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1442
LENGTH: 523
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NAME/KEY: CDS
LOCATION: 188..472
NAME/KEY: sig peptide
LOCATION: 188..295
OTHER INPORMATION: 9CORE 7.80000019073486
OTHER INFORMATION: seq CFVLLFFLRWSLT/XC
NAME/KEY: misc_feature
                                                                                                                                           367086 ACAAGGAATTGATACCCAGAA 367066
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                                                                                                                                                                                                                                                US-09-621-976-1442/c
; Sequence 1442, Application US/09621976
; Patent No. 6639063
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
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                                                                                      61 ATTAGAGACTTCTATCCAGGA 81
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OTHER INFORMATION: n=a, g, c or t
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Maximum Match 99%
Listing first 45 summaries
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11: geneseqn1980s:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ab132117	Abk31177 Signal tr			9	Abl70131 Chemicall	Ada02552 Human WNT	Adb72290 Human WNT	Aak77730 Human imm	٠.	Ade43582 Polymorph	Ade43581 Human IDE	Ade43315 Human IDE	Aah04914 Human cDN	Aah17530 Human cDN	Continuation (3 of	Abk53951 Human hea	Abk54007 Human hea	Abk54004 Human hea	Abk54001 Human hea	Aaz24559 Human lun	Aac65798 Human lun	Abl49017 Human lun
COLUMNIA	D	ABL32117	ABK31177	ABL70132	ABL32116	ABK31176	ABL70131	ADA02552	ADB72290	AAK77730	AAK77731	ADE43582	ADE43581	ADE43315	AAH04914	AAH17530	ADE11169 2	ABK53951 ⁻	ABK54007	ABK54004	ABK54001	AAZ24559	AAC65798	ABL49017
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æ	Query	74.6	74.6	74.6	72.3	72.3	72.3	62.0	62.0	58.5	58.5	58.5	58.5	58.5	58.0	58.0	57.3	56.5	56.5	56.5	56.5	56.5	56.5	56.5
	Score	09	60.4	60.4	58.6	58.6	58.6	50.2	50.2	47.4	47.4	47.4	47.4	47.4	47	47	46.4	45.8	45.8	45.8	45.8	45.8	45.8	45.8
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and

Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.

Claim 1; SEQ ID NO 90; 32pp + Sequence Listing; German.

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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disciplinte. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the disgnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell insue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                             9541 TCAAAAAATAAAACACAAACCCGCAAAACAATAAAAATATCTATAAATCATATATCCG 9482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                      1 TCAAGAAAGTGAAAACACACAGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal transduction associated gene modified complementary DNA #10.
                 leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                 Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                                                                                                                                                                ö
                                                                                                                                   / Match 74.6%; Score 60.4; DB 6; Length 13249; Local Similarity 85.9%; Pred. No. 8.6e-10; les 67; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 20; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK31177 standard; DNA; 13249 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-147896/19.
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signaling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligomuclectides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as social tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                        9482
                                                                                                                                                                o;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
       sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                        9541 TCAAAAAAATAAAAACACGCGCAAAAACAATAAAAATATCTATAAATGTATCCG
                                                                                                                                                                                                     1 TCAAGAAAGTGAAAACACACACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
sequences. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemically treated cell signalling DNA sequence complementary to#11.
                                                                                         Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                                                                                                                                                0,
                                                                                                                             Length 13249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 22; 24pp + Sequence Listing; English.
                                                                                                                             4; DB 6;
8.6e-10;
with signal transduction, or their complementary
                                                                                                                                                                0; Mismatches
                                                                                                                             74.6%; Score 60.4; 85.9%; Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                78
                                                                                                                                                                                                                                                                                                                                                                                                       ABL70132 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001; 2001WO-EP007471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                             61 ATTAGAGACTTCTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                               Local Similarity 85.9
es 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-154758/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200202807-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL70132;
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
ABL70132/c
                                                                                                                                                   Best Loca
Matches
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sapiens.
                                                                                                                                                                       23-APR-2002
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                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                               ABK31176;
          3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                  olek A,
                                                                                                           ABK31176
                                                                                               RESULT
                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebuxaemia, Alzheimer's disease, Alz, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                ó
                                                                                              9541 TCAAAAAATAAAAACCCACAAAAACAATAAAATATCTATAAATCATATATCCG 9482
                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; antiaHIV; anticonvulant; ophthalmologic; antitheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinfleumatory; cancer; eye disease; arteriosclerosis; anamia; autiinfleumatory; cancer; eye disease; atteriosclerosis; anamia; autiente myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurotibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                       1 TCAAGAAAGTGAAAACACCACAGCAGCAATAAAATGTCTGTAAGTCATGTATCCG
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 72.3%; Score 58.6; DB 6; Length 13249; Similarity 82.7%; Pred. No. 3.3e-09; 67; Conservative 0; Mismatches 14; Indels 0;
Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                               ..
                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 89; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 89.
                       Score 60.4; DB 6;
Pred. No. 8.6e-10;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                             ABL32116 standard; DNA; 13249 BP.
                                                                                                                                                9481 ATTAAAACTTCTATCCA 9464
                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP007537.
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01-SEP-2000; 2000DE-01043826.
                        74.6%;
85.9%;
                                                                                                                         ATTAGAGACTTCTATCCA
                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-130909/17
                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methylation.
                                                61;
                                                                                                                                                                                                                                       ABL32116;
                        Query Match
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                                       Local
                                                  datches
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically condition of bisulphite, hydrogen sulphite or disulphite.

Also disclosed are oligonuclectides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method contained state associated with signal transduction. The genomic DNA can be contained from cells or cellular components which contain DNA, e.g. cell cines, biopsies, blood, sputum, stool, wine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction, or their complementary sequences. Note: The sequence of the fivention are chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 72.3%; Score 58.6; DB 6; Length 13249; Local Similarity 82.7%; Pred. No. 3.3e-09; les 67; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal transduction associated gene modified DNA #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 19; 24pp; English.
                                                                                                                                                                                                                          ATTAGAGATTTTTATTTAGGA 3789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
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                                                                                                                                                  61 ATTAGAGACTTCTATCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK31176 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-2001; 2001WO-EP007472.
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01-SEP-2000; 2000DE-01043826.
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Local Similarity

Matches

Query Match

3769 ATTAGAGATTTTTATTAGGA 3789

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RESULT 7

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The invention relates to a nucleic acid comprising a sequence of at least seases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonate for PNA-oligomers for particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL/0111-ABL/0626 represent chemically pre-treated genemic DNA so f genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed sequence information supplied by the
               3709 TTAAGAAAGTGAAAATATATTCGTAGAAGTAATAAAAATGTTTGTAAGTTATGTATTCG 3768
                                                                                                                                                                                                                                                                                                                                 Cell signalling; cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 21; 24pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                Chemically treated cell signalling DNA sequence#11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
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Pred, No. 3.3e-09;
                                                                                           3769 Arradadarrirriarradda 3789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin K;
                                                        81
                                                                                                                                                                                     ABL70131 standard; DNA; 13249 BP.
                                                          61 ATTAGAGACTTCTATCCAGGA
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82.7%;
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                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                         tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200202807-A2
                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
                                                                                                                                                                                                                                                             01-JUL-2002
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3709 ITAAGAAAGIGAAAATATAATICGIAGAAAGITAATAAAAIGITIGITIGITATIGIATITG 3768

61 ATTAGAGACTICTATCCAGGA 81

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1 TCAAGAAAGTGAAAACACACACGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60

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Gaps

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14; Indels

0; Mismatches

Conservative

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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic trans-acting viral genes, meaning that cancer incidence is a trandom. Many of these do not carry transduced host oncogenes or compensity transduced host oncogenes or direct consequence of the effects of provintal integration into host corcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therepoutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this control of format dianot format directly from a proper in the printed specification, but was obtained in all performing forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36015 TCAAGCAAGTGAAAAGACAACCCACAGAATGGGGGAAAATATTTGCAAGTCATGTATTGG 35956
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                                                                                                                                                                          Human, carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 72332 BP; 16680 A; 18843 C; 19431 G; 16654 T; 0 U; 724 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.2; DB 8; Length 72332; Pred. No. 2.5e-06;
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                                                                                                                                 Human WNT3A carcinoma associated gene, SEQ ID NO:1070.
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              ADA02552 standard; DNA; 72332
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                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2001; 2001US-00035832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-587068/55.
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                                                                                                                                                                                                                                                                                                 WO2003057146-A2.
                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                           06-NOV-2003
                                                                                                                                                                                                                                                                                                                                         17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morris DW;
                                                                                                                                                                                                                  gene; ds.
                                                       ADA02552;
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ADA02552/c
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                    cytostatic; gene therapy; vaccine; metastasis; ds
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2000US-0225213P.
2000US-0225214P.
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2000US-0225267P.
2000US-0225268P.
2000US-0225270P.
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2000US-0225757P.
2000US-0225758P.
2000US-0225759P.
2000US-0226739P.
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2000US-0229344P.
2000US-0229345P.
2000US-0229509P.
2000US-0229513P.
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2000US-0232081P.
2000US-0231968P.
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2000US-0184664P.
2000US-0186350P.
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2000US-0227182P.
2000US-0227009P.
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2000US-0220963P.
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2000US-0229287P
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                                                                                                                                                                            2000US-0189874P
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                                                                                                          17-JAN-2001; 2001WO-US001354
                                                               WO200157182-A2
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                                          Homo sapiens.
                                                                                                                                                                                                                                         30-JUN-2000;
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                                                                                                                                                                                                                    07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                             4-AUG-2000;
                                                                                     09-AUG-2001
TCAAGCAAGTGAAAAGACAACCCACAGAATGGGGGAAAATATTTGCAAGTCATGTATTGG 35956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 60 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, another neoples and adenocarcinoma, and sarcommas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                  recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 72332 BP; 16680 A; 18843 C; 19431 G; 16654 T; 0 U; 724 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32542
                                                                                                                                          human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50.2; DB 9; Length 72332;
Pred. No. 2.5e-06;
0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                             cancers, neoplasm, adenocarcinoma, or sarcomas
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 118; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AXX77730/c
1D AAK77730 standard; DNA; 16532 BP. XX
AC AAK77730; XX
XX
DT 07-NOV-2001 (first entry)
XX
XX
DE Human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAAGGGACTIGTATGCAG 35937
35955 ATAAGGGACTTGTATGCAG 35937
                                                      BP
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                                                     72332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTAGAGACTTCTATCCAG
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23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-0052482.
30-NOV-2001; 2001US-00937722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                           26-DEC-2001; 2001WO-US051291.
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                            (first entry)
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hes 61; Conservative
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R. 21-SEP-2000; 2000UG-023497P. PR 25-SEP-2000; 2000UG-023497P. PR 26-SEP-2000; 2000UG-023494P. PR 26-SEP-2000; 2000UG-023544P. PR 27-SEP-2000; 2000UG-023544P. PR 27-SEP-2000; 2000UG-023544P. PR 27-SEP-2000; 2000UG-023546P. PR 29-SEP-2000; 2000UG-023546P. PR 29-SEP-2000; 2000UG-023546P. PR 29-SEP-2000; 2000UG-023636P. PR 29-SEP-2000; 2000UG-023636P. PR 29-SEP-2000; 2000UG-023636P. PR 29-C-CT-2000; 2000UG-023636P. PR 02-CT-2000; 2000UG-023636P. PR 02-CT-2000; 2000UG-023636P. PR 13-CT-2000; 2000UG-023139P. PR 20-CT-2000; 2000UG-024652P. PR 20-CT-2000; 2000UG-024652P. PR 20-NOV-2000; 2000UG-024921P. PR 20-NOV-2000; 2000UG-024929P. PR 20-NOV-2000; 20
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) anno acid sequences given in AAM92170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or delactions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the concleic acids into a host cell and culturing the used to prevent, (I) proteins and polymucleotides may be used to prevent, (I) diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invantion. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4021 TCAAAAAGTGAAAAGACAACTCACAGAAAGGAAGAAAATATTTGCAAATCATGTATCTG 3962
                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCAAGAAAGTGAAAAACACAAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 32542; 3071pp + Sequence Listing; English.
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2000US-0180628P.
2000US-0184664P.
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2000US-0189874P
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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AAK77731/c
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PR 17-MR-2000; 2000US-0190076P.
PR 18-ARR-2000; 2000US-019912P.
PR 18-ARR-2000; 2000US-020954FP.
PR 28-UJM-2000; 2000US-0215185P.
PR 70-UJM-2000; 2000US-0215185P.
PR 70-UJM-2000; 2000US-0216486FP.
PR 11-UJL-2000; 2000US-021648FP.
PR 14-UJL-2000; 2000US-021749FP.
PR 14-UJL-2000; 2000US-021749FP.
PR 14-UJL-2000; 2000US-022265FP.
PR 14-AUG-2000; 2000US-022265FP.
PR 14-AUG-2000; 2000US-022256FP.
PR 16-SEP-2000; 2000US-022256FP.
PR 16-SEP-2000; 2000US-022256FP.
PR 25-AUG-2000; 2000US-022256FP.
PR 25-AUG-2000; 2000US-022256FP.
PR 25-AUG-2000; 2000US-022256FP.
PR 25-SEP-2000; 2000US-022325FP.
PR 16-SEP-2000; 2000US-022325FP.
PR 16-SEP-2000; 2000US-022325FP.
PR 16-SEP-2000; 2000US-023235FP.
PR 16-SEP-2000; 2000US-023325FP.
PR 16-SEP-2000; 2000US-023325FP.
PR 16-SEP-2000; 2000US-023325FP.
PR 16-SEP-2000; 2000US-023325FP.
PR 25-SEP-2000; 2000US-023335FP.
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Ruben SM
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17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
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17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
10-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
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2000US-0249208P.
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2000US-0249214P.
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  13-OCT-2000;
20-OCT-2000;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 32543; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen [I]

amino acid sequences given in AAK92170 to AAK91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

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     proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the nucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers metastases of haematopoietic antigen genomic sequences from the present invention. AAK64912 to AAK87691 and AAM82169 ceptences to the present invention of the present invention
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                                                                                                                                                                                                                                                          Sequence 16535 BP; 4440 A; 3253 C; 3307 G; 5535 T; 0 U; 0 Other;
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"There is a variation at this position"
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"There is a variation at this position"
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                                                                                                                                                   Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 128034 BP; 34726 A; 25977 C; 26400 G; 40799 T; 0 U; 132 Other;
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                                                                                            Bertram L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                            Tanzi RE,
                                                                                            Wang X, Ta
                                                                                                                                                                                                                Claim 9; Page 584-page 618; 848pp; English
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                                                                                             Elliott KJ,
                                                                                                         Sampson AJ,
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 08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-0338363P.
04-DEC-2001; 2001US-0337052P.
28-MAR-2002; 2002US-0368919P.
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Local Similarity 74.1%;
nes 60; Conservative
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                                                           (NEUR-) NEUROGENETICS INC. (GEHO ) GEN HOSPITAL CORP.
                                                                                            Velicelebi G,
                                                                                                        Mullin KM,
                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease.
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                                                                                                         Saunders AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from UPA (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulindegrading enzyme), KNBLI (Kinesin-like protein 1), LIPA (lysosomal acid lypase), and INFRSF6 (Tumour Necrosis Factor Receptor-SPG), where the presence of at least one of the allelic variant of one or more polymorphic regions is indicative of a predisposition for or the
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                                                                                                                                                                                                                                                         Bertram L;
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                                                                                                                                                                                                                                                             Tanzi RE,
                                                                                                                                                                                                                                                         Elliott KJ, Wang X, T. Sampson AJ, Blacker DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 549-584; 848pp; English.
                                                                                                                                                                                                                                                      Elliott KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18912 ATAAGGGACTTGTATAGAGAA 18892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTAGAGACTTCTATCCAGGA
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08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-0338363P.
04-DEC-2001; 2001US-0337052P.
                                                                                               28-MAR-2002; 2002US-0368919P
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                                                                                                                                                                                               GEN HOSPITAL CORP
                                                                                                                                                                (NEUR-) NEUROGENETICS INC
                                                                                                                                                                                                                                                             Becker KD, Velicelebi G,
Saunders AJ, Mullin KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-559131/52.
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Isogai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH17530;
                                                                                                                                                                                  Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X B X S X X X B X B X B X X X X A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104723 TCAAGAAAGTGAAAAGACAACCTATAGAATGGCATAAAATATTGTAAATGTAATATCTTATTG 104782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or an allelic variant of one or more polymorphic regions of one or more genes selected from UPA (Urokinase plasminogen activator), SNGS (gamma-synuclein), IDE (insulindegrading enzyme), KNSII (Kinesin-like protein 1), LIPA (lysosomal acid lypase), and TNRRSF6 (Tumour Necrosis Factor Receptor-SF6), where the presence of at least one of the allelic variant of one or more polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on chromosome 10. M1 is useful for determining a predisposition for or the occurrence of, and for treating neurodegenerative disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                              Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCAAGAAAGTGAAAACACACACCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                                                                                                                                                                                                                     Bertram L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 202100 BP; 60747 A; 41352 C; 41113 G; 58888 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.5%; Score 47.4; DB 9; Length 202100; 74.1%; Pred. No. 2.4e-05; ive 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                     Tanzi RE,
                                                                                                                                                                                                                                   Velicelebi G, Elliott KJ, Wang X, T, Mullin KM, Sampson AJ, Blacker DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cDNA clone (5'-primer) SEQ ID NO:1749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 769-823; 848pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104783 ATAAGGGACTTGTATAGAGAA 104803
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25-OCT-2001; 2001US-0339525F.
08-NOV-2001; 2001US-0336929P.
08-NOV-2001; 2001US-0338363P.
09-NOV-2001; 2001US-0338363F.
04-DEC-2001; 2001US-0337052P.
28-MAR-2002; 2002US-0368919P.
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                                                                                                                                                                 (NEUR-) NEUROGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease.
                                                                                                                                                                                                                                                                                                            WPI; 2003-559131/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer;
                                                                                                                                                                                                                                                           Saunders AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
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                                                                                                                                                                                                                                        Becker KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonuclectide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprises at sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide of sequence, where the
complementary strand of a polynucleotide comprises a 1-end sequence, where the
coligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in the
copperation of the primer sets can be used in antisense therapy and in
copperation and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the full-length
copperation and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
copperation and/or diagnosis of the abnormality of the primer sets and
copperation and/or diagnosis of the abnormality of the primer sets
copperation and/or diagnosis of the abnormality of the primer sets
copperation and/or diagnosis of the abnormality of the primer sets
copperation and/or diagnosis of the abnormality of the primer sets
copperation and sequences; and AAH13623 to AAH13622 represent
copperation and sequences; and AAH13629 to AAH3622 represent
copperation and sequences; and AAH13629 to the primer sets in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AAGAAAGTGAAAACACAAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 AAAAAAGTGAAAATACAACCCATAGAAAGATAAAAAATATTTTCAAGCCATGTATCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                             Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1749; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 4; Length 752; Pred. No. 1.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                             Saito K,
Otsuki
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                                                                                                                                                                                                                                                                                                             Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                             Wakamatsu
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                                                                                                                                                                                                                                                                                                    sogai T, Nishikawa T,
Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH17530 standard; cDNA; 1794
27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MRY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 58.0%;
1 Similarity 74.7%;
59; Conservative
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                                                                                                                                                                                                                             (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
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Best Local Similarity
Matches 59; Conserv
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                     Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                 29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAXY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                 28-JUL-2000; 2000EP-00116126.
                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                WPI; 2001-318749/34.
07-FEB-2001
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The present invention describes primer sets for synthesising 5602 full
[1] an oligo-dr primer and an oligonuclectide complementary to the

[2] complementary strand of a polynuclectide comprises one of the 5602

[3] an oligonuclectide comprises at least 15 nuclectides; or (b) a compination

[3] complementary strand of a polynuclectide which comprises one of the 5602

[4] an oligonuclectide comprising a sequence complementary to the

[5] complementary strand of a polynuclectide which comprises a 5'-end

[6] complementary strand of a polynuclectide which complementary to the

[5] complementary strand of a polynuclectide which complementary to the

[6] complementary strand of a polynuclectide which complementary to a

[7] complementary strand of a polynuclectide which complementary to a

[7] complementary strand of a polynuclectide which complementary to a

[8] complementary strand of a polynuclectide of sequence complementary to a

[8] complementary strand of a polynuclectide of sequence, where the

[8] complementary strand of a polynuclectide of the abnormality of the primers are also useful for the complement of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AMH3632 represent thuman amino acid sequences, and AMH3632 to AMH3632 represent thuman amino acid sequences, and AMH3632 to AMH3632 represent the primers and a polynuclectide of the polyn Claim 8; SEQ ID NO 17007; 2537pp + Sequence Listing; English.

Sequence 1794 BP; 665 A; 328 C; 368 G; 433 T; 0 U; 0 Other;

58.0%;

3 AAGAAAGTGAAAACACAAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT 62 0; Gaps Score 47; DB 4; Length 1794; Pred. No. 1.4e-05; 0; Mismatches 20; Indels 0; Mismatches 59; Conservative Query Match Best Local Similarity Matches 59; Conserv

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Search completed: May 7, 2004, 13:50:26 Job time: 168.476 secs

AQ349913 RPCIII-12 CC489556 CH240.322 CE520001 tigr-9ss-AQ106226 H3 3070.A CE533552 tigr-9ss-AQ106326 H3 3070.A CE533552 tigr-9ss-BZ387096 EINCM29TF AQ0887236 HS 5552.B AZ0887236 HS 5552.B AZ0887236 HS 5552.B AZ08859 RXC11-15 AQ88723979 qA44d09.x BX098859 RX099859 BV763852 saa48h09. AW183073 x56605.x BE041580 hos512.x AW183073 x56605.x BE041580 hos512.x AW183073 x6605.x CE299189 tigr-9ss-CE299189 tigr-9ss-CE299189 tigr-9ss-CE299189 tigr-9ss-CE299189 tigr-9ss-CE299189 tigr-9ss-CE299189 tigr-9ss-CC20210389 H32 51.C0 CE104592 tigr-9ss-AV28536 LG1 285 G BZ339389 ic31h04-9 CC0210389 HS1 51.C0 CB084591 hq18b10.b BHZ03848 SM1-44X7. CD75210389 HS153309 CC676317 OGUDB34TV AQ534651 RPCI-11-3 CC676317 RPCI-11-3 CC676317 RPCI-11-3 CC676317 RPCI-11-3 AQ5350425 Danio rer

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CG45299
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BAZ387096
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CC471346
AIC39979
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CC2911346
AW8332
CC291333389
CC6203324

419 521 557 672 678

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AQ164003 113 bp DNA linear GSS 16-OCT-1998 HS 2270_Bl_E07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=13 Row=J, genomic survey
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 313)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
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AQ164003.1 GI:3562198
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Homo sapiens
$\text{Results of $\text{Resul
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AUTHORS
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AQ442281 HS_5137_A
CE266277 tigr-9885-
CC535951 CH240_414
                                                                                                            7, 2004, 13:34:53 ; Search time 934.416 Seconds (without alignments) 1629.864 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                         27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                        Notal number of hits satisfying chosen parameters:
                                                                                                                                                                     US-10-071-411A-1_COPY_450_500
51
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AQ442281
CE266277
CC535951
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                                                                                 nucleic search, using sw model
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Perfect score:
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University of Mashington
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Gueen Anne Ge-3618
Fax: (206) 616-3868
Email: jwallace@u.washington.edu
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availablity, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 713 row: M column: 13
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1 (bases 1 to 416)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Feller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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Homo sapiens
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                                                                                                                                                                                                                                                                             /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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HS_5137_A1_G07_SP6E_RPCI-11 Human Male BAC Library Homo sapien
genomic_clone Plate=713 Col=13 Row=M, genomic survey sequence.
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/mol_type="genomic DNA"
/db xxef="texon:9606"
/clone="Plate=713 Col=13 Row=M"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 28; Length 313;
Pred. No. 2.8;
0; Mismatches 10; Indels
                                                                                                                                                             1.313

"Organism="Homo sapiens"

/mol_type="@enomic DNA"

/db_xref="taxon:9606"

/clone="Plate=2270 Col=13 Row=J"
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2270 row: J column: 13
Class: BAC ends
High quality sequence stop: 313.
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Location/Qualifiers
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nilarity 80.0%;
Conservative 0
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Best Local Similarity
The 40; Conserva
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AQ442281/c
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CC535951 815 bp DNA linear GSS 17-JUN-2003 CH240 414P12.T7 CHORI-240 Bos taurus genomic clone CH240_414P12, genomic survey sequence.
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The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
/note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                                        123 bp DNA linear GSS 26-SEP-20. Jir-gss-dog-17000337092175 Dog Library Canis familiaris genomic, CE266277
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Canis familiaris
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K. Fusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9615"
/clone lib="bog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
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                                                                                                                                 DB 28;
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80.0%; Pred. No. 26;
rative 0; Mismatches
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Pred. No. 28;
0; Mismatches
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/strain="Standard Poodle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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ilarity 80.0%;
Conservative 0
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Bos taurus (cow)
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CC535951.1
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Matches 36; Conserv
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MEDLINE
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KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                  RESULT 3
CE266277
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KEYWORDS
SOURCE
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 382)

RS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.

Use of EAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building (1997)

Orber GSS: RPCII1-120E14.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buifalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buifalo.edu/ordering) or from
RACPAC Resources (http://bacpac.med.buifalo.edu/ordering) or from
Research Genetics (info@resegen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Location.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ349913
RPCII1-120E14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-120E14, genomic survey sequence.
                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site 1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
                                                                                                      9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AAAAGAAATIGGACTIAAAGITAAAIACITITGIGCITCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.4%; Score 29.8; DB 28; 82.9%; Pred. No. 47; 1ive 0; Mismatches 7;
                                                                                      The Institute for Genomic Research
                           Contact: Mark Adams
Department of Bukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell_type="Lymphocytes"
clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA'
/db_xref="GDB:7513121"
/db_xref="taxon:9606"
/clone="RPCI-11-35C18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Other GSSs: RPCI11-35C18.TJ
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AQ349913.1 GI:4177248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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Best Local Similarity
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AQ349913/c
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 491)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rboledogge.ca
Email: rboledogge.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by GSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 414 row: P column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 bp DNA linear GSS 14-APR-1999 RPCI11-35C18.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35C18, genomic survey sequence.
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                                                                                                               Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Hasi,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Ghan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Other GSSs: CH240_414P12.TARBAC13P2
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Blood"
/clone_lib="CHORI-240"
/clone_lib="CHORI-240"
/clone="Vector: pTARBAC1.3; Site_l: MboI; Site_2: MboHote="Vector: pTARBAC1.3; Site_l: MboI, Site_2: MboI Herefood bull Li Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                     The British Columbia Cancer Agency Genome Science Centre GNO W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6 Tel: 604-877-6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 AAAAAACAGGATTTCATTAAAGTTAAAAACTTTTGTACTTCAAAGAACAT 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 29; Length 815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.2%; Score 30.2; D
Best Local Similarity 74.5%; Pred. No. 33;
Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9913"
/clone="CH240_414P12"
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
/cell_type="
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SOUTCE

FEATURES

RESULT 5 AQ047026/c

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DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL

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Gaps

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CE454299 479 bp DNA linear GSS 27-SEP-2003 tigr-gss-dog-17000319453122 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kirkness EF
The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tal: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (dog)

Canis familiaris

Canis familiaris

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.

I (Dases I to 642)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               642 bp DNA linear GSS 28-SEP-20 genomic, genomic, genomic survey sequence.
/note="Vector: pTARBAC1.3; Site 1: Mbo1; Site 2: Mbo1; Hereford bull L1 Domino 99375; GHOR1-240 Bovine BAC library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/db xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                  Length 809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                348 agarararaaacregacrraaaargaaaarriririsiscritsara 304
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                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Canis familiaris"
                                                                                                                                                                                          DB 7
                                                                                                                                                                                                      56.9%; Score 29; DB 77.8%; Pred. No. 75; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence
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                                                                                                                                                                                                                                                                                     35; Conservative
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Best Local Similarity
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PUBMED
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Email: rholt@bcggc.ca

Clones are derived from the bovine BAC library CHGRI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering information.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

British Columbia Genome Sciences Centre, Canada.

Plate: 322 row: D column: 15

Seg primer: T7

Class: BAC ends.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                          /db_xref="taxon:9606"
/clone="RPCI-11-120B14"
/cst="Male"
/cell_type="Lymphocytes"
/clone_lab="RPCI-11"
/clone_lab="RPCI-11"
/nore="Tvccor: pBACc3.6; Site_1: EcoR1; Site_2: EcoR1;
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z
Tel: 604-877-6085
Fax: 604-877-6276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.9%; Score 29; DB 28; Length 382; 77.8%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 AAATAGATAAATTGGACTTAATTTTAAAAACGTGTGTGCCTCAAA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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/strain="breed: Hereford"
                                                                       'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="GDB:7545805"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9913"
/clone="CH240_322D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Conservative
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Matches 35; Conserv
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CC489556/c
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JOURNAL
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Gaps

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BZ387096 841 bp DNA linear GSS 30-APR-2003
BINCM29TF BI_10_12_KB Entamoeba invadens genomic clone EINCM29,
genomic survey sequence.
BZ387096.1 GI:30233424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tal: 301-838-0208
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 28-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.

1 (bases 1 to 669)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, DB., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                     669 bp DNA linear GSS 28-SEP-20. tigr-ges-dog-17000366522943 Dog Library Canis familiaris genomic, CEE593552
                                                                     /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9615"
/clone lib="Dog Library"
/note="Site l: BstXI; Libraries were prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                     0
                                                                                                                                                                                          55.3%; Score 28.2; DB 28; Length 265; 80.5%; Pred. No. 1.5e+02; ive 0; Mismatches 8; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGC 39
                                                                                                                                                                                                                                                                                    4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.5%; Score 27.8; DB 29;
Best Local Similarity 82.1%; Pred. No. 1.8e+02;
Matches 32; Conservative 0; Mismatches 7;
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/dboe="plate=3070 Col=8 Row=1"
/exx="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CE593552.1 GI:36910333
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Canis familiaris
                                                                                                                                                                                                                                       33; Conservative
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ORGANISM
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CE593552
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1 (bases 1 to 265)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Haler, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS 28-AUG-1998
                                                                                                                                                                                          Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Pax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ106326
HS_3070_A2_E04_MR_CIT_Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3070 Col=8 Row=I, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                    1 (bases 1 to 479)
Kirknes, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K. Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone lib="Dog library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                           The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
    Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: (Wallace@u.washington.edu
Sequence Tagged Connector
Plate: 3070 row: I column: 8
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.6; DB 29; Length 479;
Pred. No. 1.1e+02;
0; Mismatches 9; Indels 0
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             Email: ekirknes@tigr.org
Class: shotgun.
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AQ106326.1 GI:3481682
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1 Similarity 79.1%;
34; Conservative C
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AQ386453/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        646 bp DNA linear GSS 02-NOV-200 Pan troglodytes DNA, clone: PTB-028L09.R, genomic survey sequence. AG048782 AG048782.1 GI:16585674 GSS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Fuljyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Tocoki, Y., Maranabe, H. and Sakaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center Drive, Rockville, MD 20850, USA
                                                        Entamoeba invadens
Eukaryota, Entamoebidae; Entamoeba.

1 (Bases 1 to 841)
Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Bellen,K., Hall,W., Anderson,I. and Loftus,B.
Gene discovery in the Entamoeba invadens genome Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seg primer: TF
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Contact: Brendan Loftus
Department of Eukaryotic Genomics
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/mol_type="genomic DNA"
/strain="IP-1"
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Location/Qualifiers
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Fax: 301-838-0208
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RPCIII-154D12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-154D12,
AQ386453
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please context Pieter de Jong
Library availability, please context Pieter de Jong
(pieter@dejong.med.bufalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
http://www.tigr.org/tdb/humgen.bac_end_search/bac_end_search.html
Seg primer: T7
Class: BAC ends.
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1 (bases 1 to 700)
Zhao, Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
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Unpublished (1997)
Unpublish
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC
was generated during the R&D process and may have higher chance
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/db_xref="taxon:9598"
/clone="PTB=028L09.R"
/sex="male"
/cell_type="lymphoblast"
/cell_type="lymphoblast"
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Pred. No. 2.3e+02;
0; Mismatches 11;

    . .646
    /organism="Pan troglodytes"

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/db_xref="GDB:7558835"
/db_xref="taxon:9606"
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1. .700
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R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                             Sequencing: M13Rev
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                                                                                                                                                          clone tracking errors.
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ilarity 75.6%;
Conservative (
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Homo sapiens
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Loract: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Gloss are derived from the human BAC library RPCI-11. For BAC
701 Clones are derived from the human BAC library RPCI-11. For BAC
701 Library availability, please contact Fieter de Jong
701 Library availability, please contact Fieter de Jong
702 Library availability, blease contact Pieter de Jong
703 Library availability, blease contact Pieter de Jong
704 Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
705 Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
706 Resources (http://www.htsc.washington.edu
707 Blate: 9320 row: J column: 6
708 Drimer: 8P6
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector back as isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 449)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                               AQ887236
HS 5552 B2 E03 SPGE RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=9320 Col=6 Row=J, genomic survey sequence.
                                                                                                                                                                                         ö
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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                                                                                                                                   Length 700;
                                                                                                                                                                                                                                                                                    545 ATATAGATAAATTGGACTTCAATAAAATTACTTGTGTGCGCAAA 501
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                                                                                                                                     53.7%; Score 27.4; DB 28; Length 75.6%; Pred. No. 2.3e+02; Artive 0; Mismatches 11; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=9320 Col=6 Row=J"
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High quality sequence stop: 449.
Location/Qualifiers
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Best Local Similarity
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ORGANISM
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KEYWORDS
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4 AAAAGAAATIGGACTTAAAGTIAAATACTTTTGTGCTTCAA.44

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253 ATAACAGACTGAACTTAATGTTAAAAAANTNTTGTGCTTCAA 293
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Search completed: May 7, 2004, 15:42:23 Job time : 943.083 secs

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Query Match
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Sequence 224858,
Sequence 224858,
Sequence 27417, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 323533,
Sequence 323533,
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Sequence 103827
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2194,362 Million cell updates/sec
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                                                                                                                                                                           51
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                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications Na;

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'cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
'cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-027-623-224858
US-09-960-870-7
US-09-960-858-7
US-10-251-668-7
US-10-205-220-1
US-10-027-633-33533
US-10-027-633-33533
US-10-027-633-103827
US-10-027-632-103827
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Maximum Match 99%
Listing first 45 summaries
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Sequence 235079,
Sequence 1414, Ap
Sequence 1393, Appl
Sequence 31332, A
Sequence 45, Appl
Sequence 268, Appl
Sequence 268, Appl
Sequence 36924, Appl
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Sequence 7470, Ap
Sequence 82, Appl
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Sequence 75, Appl
Sequence 57, Appl
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Sequence 297,
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1 US-09-984-429-344
3 US-10-07-632-235079
3 US-10-027-632-235079
5 US-10-027-632-235079
5 US-10-21-455-1414.
5 US-10-240-452-62
6 US-10-22-798-1332
6 US-10-242-798-31332
6 US-10-242-417-45
7 US-09-764-847-268
7 US-10-027-632-36924
7 US-09-764-847-268
8 US-10-027-632-36924
9 US-10-027-632-369812
9 US-10-027-632-369812
9 US-10-027-632-369812
9 US-10-027-632-32541
9 US-09-994-300-57
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US-10-311-455-11111
US-09-764-891-7470
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US-10-027-632-224858

US-10-027-632-224858

Sequence 224858, Application US/10027632

Publication No. US203030204075A9

GENERAL INFORMATION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 1099-11-23

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 224858

LENGTH: 605
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                                  DB 13;
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                              58.4%; Score 29.8; Dilarity 79.1%; Pred. No. 12; Conservative 0; Mismatches
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robe
Query Match
Best Local Similarity
Them 34; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-282-122A-27417/c
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ORGANISM: Human
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APPLICANT:
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                                              Sequence 90, Application US/10311455

Sequence 90, Application US/203143608A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander:

APPLICANT: DIER, Alexander:

APPLICANT: DIER, Alexander:

APPLICANT: DIER, Alexander:

APPLICANT: DIER, ALEXANDER:

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT APPLICATION NUMBER: US/201.07.537

PRIOR FILING DATE: 2001-07.02

PRIOR FILING DATE: 2001-06-30

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR PLING DATE: 2000-06-30

RIOR PLING DATE: 2000-06-30

RIOR FILING DATE: 2000-06-30
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/01/06/05

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-20

PRIOR FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,218

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1099-103-24

PRIOR FILING DATE: 1099-103-24

PRIOR FILING DATE: 1999-103-24

PRIOR FILING DATE: 1999-103-28

PRIOR FILING DATE: 1999-003-28

PRIOR FILING DATE: 1999-003-08

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 224858, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
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| OTHER INFORMATION: n = A,T,C or G
US-10-027-632-224858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-027-632-224858
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                                              US-10-311-455-90/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 13249
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Matches
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TYPE: DNA
) ORGANISM: M. genitalium
US-10-251-668-7
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; ORGANISM: M. genitalium
US-09-960-858-7
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US-10-251-668-7/c
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FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 06/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-24

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-06

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-26

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-03-06

PRIOR PRIOR
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Publication No. US20030134281A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BVANS, Glen
TITLE OF INVENTION: USE
FILE REPERBNCE: P.EA 4738
CURRENT APPLICATION NUMBER: US/09/960,870
CURRENT APPLICATION NUMBER: 2001-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycoplasma genitalium
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Best Local Similarity 72.3%
Thes 37; Conservative
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Matches 37; Conservative
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US-09-960-870-7
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US-09-960-858-7/c
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US-09-960-870-7/c
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LENGTH: 879
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Sequence 7, Application US/09960858

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Sequence 1, Application US/10205220
Publication No. US20030170663A1
GENERAL INFORMATION:
TITLE OF INVENTION: Mucleotide Sequence of the Mycoplasma Genitalium Genome, Fragmer TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB193PLD1
CURRENT APPLICATION NUMBER: US/10/205,220
CURRENT APPLICATION NUMBER: US 08/545,528
PRIOR PRILING DATE: 1995-06-07
PRIOR PLING DATE: 1995-06-07
PRIOR PLING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
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                                                                                                                                                                                                                                                                                                                                                                            Length 10809;
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; Bublication No. US20040063097A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glan
; TITLE OF INVENTION: USE
; FILE OF INVENTION: USE
; FILE REFERENCE: P-RS 5441
; CURRENT APPLICATION NUMBER: US/10/251,668
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/960,607
; PRIOR APPLICATION NUMBER: US 09/960,607
; RIUNGER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
: LENGTH. 10809
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EVANS, Glen
TITLE OF INVENTION:
TITLE OF INVENTION: USE
FILE REPRENCE: P-EA 4974
CURRENT APPLICATION NUMBER: US/09/960,858
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 10809
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Pred. No. 59;
O; Mismatches
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Pred. No. 59;
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72.5%;
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Best Local Similarity 72.5%;
Matches 37; Conservative
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Best Local Similarity 72.5
Matches 37; Conservative
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Gaps

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: U5/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                               51.4%; Score 26.2; DB 13; Length 493; 72.3%; Pred. No. 1.5e+02; ive 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                   2 CAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACAT 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification and Mapping of Single ITILE OF INVENTION: Pollymorphisms in the Human Genome FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-24

PRIOR PELING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/186,388

PRIOR PELING DATE: 1999-10-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-20-88

PRIOR FILING DATE: 1999-10-80-80

NUMBER OF SEQ ID NOS: 325720

SOFTWARRE: FastSEQ FOR Windows Version 4.0

LENGTH: 493
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Pred. No. 1.5e+02;
0; Mismatches 13;
; NUMBER OF SEQ ID NOS: 325720
; SOFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 323533
; LENGTH: 493
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-323533
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 323533, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 72.3
Matches 34; Conservative
                                                                                                                                                                                                                                                                           Best Local Similarity 72.3
Matches 34; Conservative
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 8350
                                                                                                                                                                                                                                                                              0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Learning in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR RIPLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1000-03-29
PRIOR PILING DATE: 1099-10-23
PRIOR PILING DATE: 1000-03-29
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                                                                                                                                                                                                               Score 28.6; DB 15; Length 580073;
Pred. No. 1.6e+02;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                       TCAAACATCAT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_10754C.1
US-10-424-599-8350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 323533, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8350, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                              ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
                                                                                                                                                                                                            vuery Match
Best Local Similarity 72.5%;
Matches 37; Conservative
      SOFTWARE: PatentIn version 3.1
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US-10-027-632-323533/c
                                  SEQ ID NO 1
LENGTH: 580073
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US-10-424-599-8350
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publication No. US2003024075A9

publication No. US2003024075A9

GENERAL INFORMATION:

APPLICANT Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR PRILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-108-08

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.4%; Score 26.2; DB 13; Length 1371; 72.3%; Pred. No. 1.9e+02; ive 0; Mismatches 13; Indels 0;
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
SEQ ID NO 103827
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103827
LENGTH: 1371
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US-09-984-429-344
; Sequence 344, Application US/0998429
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Best Local Similarity 72.34
Matches 34; Conservative
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Best Local Similarity 72.3
Matches 34; Conservative
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US-10-027-632-103827/c
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; ORGANISM: Human
US-10-027-632-103827
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US-10-027-632-103827
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| Publication No. US20040010132A1
| GREMEAL INPORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: 53 Human Secreted Proteins
| TITLE OF INVENTION: 53 Human Secreted Proteins
| CURRENCE: PROJECT | 2001-10-30
| CURRENT APPLICATION NUMBER: US/09/984,429
| CURRENT APPLICATION NUMBER: 00/244,591
| PRIOR APPLICATION NUMBER: 00/210-30
| PRIOR APPLICATION NUMBER: PCT/US88/143
| PRIOR APPLICATION NUMBER: PCT/US88/1462
| PRIOR APPLICATION NUMBER: PCT/US88/1463
| PRIOR PLING DATE: 1997-10-09
| PRIOR PRIOR PLING DATE: 1997-10-09
| PRIOR PLING DATE: 1997-10
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Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 1069, App
Sequence 690, App
Sequence 690, Appli
Sequence 1278, Appli
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Sequence 35, Appl
Sequence 330, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 17, Appli
Sequence 1770, Appli
Sequence 172, Appli
Sequence 172, Appli
                                                                               May 7, 2004, 13:35:03 ; Search time 25.6094 Seconds (without alignments) 1105.159 Million cell updates/sec
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1 acaaaaagaaattggactta......ttttgtgcttcaaacatcat
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(GgnZ_6/ptodata/2/ina/5A_COMB.seq:*

(GgnZ_6/ptodata/2/ina/5B_COMB.seq:*

(GgnZ_6/ptodata/2/ina/6A_COMB.seq:*

(GgnZ_6/ptodata/2/ina/6B_COMB.seq:*

(GgnZ_6/ptodata/2/ina/PcTuS_COMB.seq:*

(GgnZ_6/ptodata/2/ina/PcTuS_COMB.seq:*

(GgnZ_6/ptodata/2/ina/PcTuS_COMB.seq:*
GenCore version 5:1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-205-258-15

US-08-205-375-3

US-08-87-680A-3

US-08-976-594-1069

US-09-976-594-1069

US-09-976-594-886

US-09-976-594-886

US-09-976-594-886

US-09-976-594-886

US-09-976-594-886

US-09-976-594-886

US-09-976-594-886

US-09-976-594-886

US-09-976-594-80

US-09-976-594-80

US-09-978-978-1

US-09-117E-530

US-09-586-002-10

US-08-96-171E-530

US-08-96-171E-530

US-08-96-171E-530

US-08-96-171E-530

US-08-96-171E-530

US-08-96-171E-530

US-09-601-198-172

US-09-601-198-172

US-09-61-198-172

US-09-61-198-172

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US-09-61-198-172

US-09-61-198-172

US-09-61-1-188-172

US-09-61-1-188-172
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Maximum Match 99%
Listing first 45 summaries
                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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488.2 1018
47.8 3921
47.8 5992
47.1 1856
46.7 164976
45.9 6609
45.9 6609
45.5 1506
45.1 1998
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APPLICANT: Fracer et al.
TITLE OF INVENTION: Macleotide Sequence of the Mycoplasma Genitalium Genome, Fragmer.
TITLE OF INVENTION: Macleotide Sequence of the Mycoplasma Genitalium Genome, Fragmer.
PATENTE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PRISSR:
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR PILING DATE: 1995-06-07
PRIOR PAPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SEQ ID NOS: 1
SEQ ID NO: 1
LENGTH: 580073
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                                                                                                    15, Appl
14, Appl
3, Appli
2161, Ap
59, Appli
                                                    29, Appl
6, Appli
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17, Appl
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US-09-749-588-3

US-09-134-001C-2724

US-09-134-001C-2724

US-09-134-000C-1305

US-09-358-383C-6

US-09-358-383C-6

US-09-358-383C-17

US-09-358-383C-17

US-09-358-383C-17

US-09-358-383C-17

US-09-38-383C-17

US-09-174-674-3

US-09-171-209-59

US-09-171-209-59

US-09-134-01C-657

US-09-134-01C-657

US-09-320-721A-3

US-09-320-721A-3

US-09-320-721A-3

US-09-320-721A-3

US-09-320-721A-3

US-09-320-721A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Young et al.
ITILE OF INFURITION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4;
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                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08545528D Patent No. 6537773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
18-09-205-258-15
9 Sequence 15, Application US/09205258
9 Patent No. 6525174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 72.5
Matches 37; Conservative
  US-08-545-528D-1
   Query Match
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,020
R FILING DATE: 1997-06-06
R APLING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,895
R APLICATION NUMBER: 60/048,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,892
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/049,373
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,875
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,374
APPLICATION NUMBER: 60/048,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LING DATE: 1997-06-06
PLICATION NUMBER: 60/048,970
LING DATE: 1997-06-06
LING DATE: 1997-06-06
LING DATE: 1997-06-06
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APPLICATION WUMBER: 60/048,878
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/070,923
FILING DATE: 1997-06-06
APPLICATION WUMBER: 60/048,880
ELING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,896
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,899
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LING DATE: 1997-06-06
PLICATION NUMBER: 60/049,019
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ILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
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APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
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APPLICATION NUMBER: 60/048,897
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,963
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
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APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Sabo, Peronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRATE: California
COUNTRY: USA
ZIP: 94111-3834
ZIP: 94111-3834
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                         Length 1018;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/567,375
FILNG DATE: 04-DEC-1995
CLASSIFICATION NUMBER: US 60/004,645

PRILING APPLICATION NUMBER: US 60/004,645

PRILING DATE: 29-SEP-1995
PRIOR APPLICATION NUMBER: US 60/004,645

PRILING DATE: 19-SEP-1995
PRICE APPLICATION NUMBER: US 60/373,375
FILING DATE: 07-JUN-1995
PRILING DATE: 17-JAN-1995
ATPONEY/AGENT INFORMATION:

REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 36,774
REGISTRATION NUMBER: 37,774
REGISTRATION NUMBER: 37,77
                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                Query Match
48.2%; Score 24.6; Di
Best Local Similarity 70.2%; Pred. No. 15;
Matches 33; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-567-375-3/c
; Sequence 3, Application US/08567375
; Patent No. 5952485
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NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 1018
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                             ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-205-258-15
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NAME/KEY: CDS
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US-08-475-891A-3/C

Sequence 3, Application US/08475891A

Patent NO. 5859339

GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcedero Center, Eighth Floor
CITY: San Francisco
STRATE: California
                                                                          3456 ATAAAAAGAACTTGGATGTATAATTATGTAAATTTACGTGTTAAATATCA 3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3928 ATAAAAAGAACTTGGATGTATAATTATGTAAATTTACGTGTTAAATATCA 3879
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CTHER INFORMATION: /product= "RRK-B"
CTHER INFORMATION: /note= "Xa21 Xanthomonas Epp. disease
OTHER INFORMATION: resistance gene RRK-B from rice (Oryza
US-08-475-891A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,891A

FILING DATE: 06-JUN-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/373,375

FILING DATE: 17-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 34,774

REGISTRATION NUMBER: 36,0200

TELEFHONE: (415) 576-0300

INFORMATION FOR SEO ID NO: 3:

SEQUENCE CHARACTERISTICS:

LANDSTHEET SECONMUMICATION:

NOPEN: MANDSTHEET SECONMUMICATION:

TELEFHONE: (415) 576-0300

INFORMATION FOR SEO ID NO: 3:

SEQUENCE CHARACTERISTICS:

LANDSTHEET SECONMUMICATION:

LANDSTHEET SECONMUMICATION:

NOPEN: MANDSTHEET SECONMUMICATION:

TELEFHONE: (415) 576-0300

INFORMATION FOR SEO ID NO: 3:

SEQUENCE CHARACTERISTICS:

LANDSTHEET SECONMUMICATION:

TOTAL SECONMUMICATION:

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; Patent No. 6525174
; GENERAL INFORMATION:
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Best Local Similarity 68.0
Matches 34; Conservative
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                                                                                                                                                                                                     3456 ATAAAAAGAACTTGGATGTATAATTATGTAAATTTACGTGTTAAATATCA 3407
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Szabo, Wer-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SQUENCES: 27
CORRESPONDENCE ADDRESS: 27
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRIES California
                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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       Length 3921;
                                                                                                                                         1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                          Indels
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
Query Match 47.8%; Score 24.4; DB 2; Best Local Similarity 68.0%; Pred. No. 19; Matches 34; Conservative 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24.4; DB 2;
Pred. No. 19;
0; Mismatches 16;
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058940US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURKENT AFFLICATION DATA:

PULICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/004,645
FILING DATE: 29-SEP-1995
RICHA APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "Xa-21"
                                                                                                                                                                                                                                                                                                                                        US-08-587-680A-3/c
; Sequence 3, Application US/08587680A
; Patent No. 5977434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.0%;
Matches 34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
TYPE: nucleic acid
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Gaps

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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
                                                 TILE REPERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,895
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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PPLICATION NUMBER: 60/048,892
ILING DATE: 1997-06-06
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PPLICATION NUMBER: 60/048,970
LING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/048,896
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,884
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FILING DATE: 1997-06-06
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LING DATE: 1997-06-06
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LING DATE: 1997-06-06
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PPLICATION NUMBER: 60/048,901
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LING DATE: 1997-06-06
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Sequence 1065, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
IIILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDE
FILE REPERBNCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

PRIOR FILING DATE: 2000-10-12
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Patent No. 6673549

GENERAL INFORMATION:
GENERAL INFOR
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| NAME/KRY: misc feature
| OTHER INFORMATION: Incyte ID No. 6673549 107309.1
| NAME/KRY: unsure
| LOCATION: 433-436, 445, 447, 454, 456, 463-465, 472, 495, 498, 662, 939
| OCATION: 83, 00 other
| US-09-976-594-1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
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                               EARLIER FILING DATE: 1997-06-06
EFALLIER PEDLICATION NUMBER: 60/048,877
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/09,923
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PATCHTIN Ver. 2.0
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APPLICATION NUMBER:
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SOFTWARE: PERL Program
SEQ ID NO 1069
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-205-258-52
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Best Local Similarity
Matches 31; Conserva
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Matches 33; Conserv
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US-09-976-594-886/c
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OTHER INFORMATION: n equals a, t, c, or MAME/KEY: misc_feature.
LOCATION: (713652)...(713652)
OTHER INFORMATION: n equals a, t, c, or
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  NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c
NAME/KEY: misc_feature
LOCATION: (103998)..(10398)
OTHER INFORMATION: n equals a, t, c
NAME/KEY: misc_feature
                                                                                                                                                                                    LOCATION: (148948).
LOCATION: (148948).
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (163385). (163385)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (191989).
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (191989).
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (130938).

LOCATION: (130938).

OTHER INPORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1309418). (1309418)

OTHER INPORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (1312837). (312837)

OTHER INPORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (312993). (312993)

OTHER INPORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (319226). (319226)

OTHER INPORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (559167). (559167)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (559167). (559167)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (559167). (559167)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (559167). (56929). (OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (559241). (50992). (OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (559241). (50992). (OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (559241). (50992).
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LOCATION: (234220).(234220)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (234814).(234814)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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LOCATION: (622708) .. (622708)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (657081) .. (657081)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REPERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR PEDLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.7%; Score 23.8; DB 4; Length 1312; Best Local Similarity 80.0%; Pred. No. 27; Matches 28; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1218 AAAGAGAATTTTACATATAGTTAAATAATTTTT 1184
                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 981037.1
US-09-976-594-886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AAAAAGAAATTGGACTTAAAGTTAAATACTTTTGT 37
FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PELING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 886
LENGTH: 1312
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NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INPORMATION: n equals a, t, c, or
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc_feature
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c,
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OTHER INFORMATION: n equals a, t, c,

NAME/EXP: misc_feature

LOCATION: (98239)..(98239)

OTHER INFORMATION: n equals a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/08916421B ; Patent No. 6503729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98:
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-08-916-421B-1
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5196 ACCAAATTAATTIGTGAAAAAAAAAAAAAGACTTTCATCTTCAAACAAC 5148
                                                                                                                                                                                                                                                                                                                                                                                                         Length 6609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Indels
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 175918.15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Pred. No. 65;
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CTHER INFORMATION: a, t, c, g, or other US-09-976-594-690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LCCATION: (1)...(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09751389
Patent No. 6630334
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81.8%;
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Best Local Similarity 67.3%;
Matches 33; Conservative
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Best Local Similarity 81.8
Matches 27; Conservative
                                                                                                                                                                                         LENGTH: 6609
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
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US-09-751-389-3/c
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0; Mismatches
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t, c,
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OTHER INPORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1313224). (1313224)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (1349473). (1349473)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                              LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                        NAME/KEY: misc feature a, LOCATION: (1084830) OTHER INFORMATION: n equals a, NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
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                                                   LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals a,
NAME/FAR: misc feature
LOCATION: (779676)...(779676)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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   LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
: (1130881)..(1130881)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
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Gaps

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Sequence 1552, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
GENERAL INCORDATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOLOG7
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT APPLICATION NUMBER: 201-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 786431
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Indels

555193 AAAAAGAAAATTAATCATGCAAATATATAATTTAATGCATCAACATTAT 555243

Sequence 690, Application US/09976594 Patent No. 6673549 PAREAL INFORMATION: APPLICANT: Furness, Michael

RESULT 10 US-09-976-594-690/c

1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51

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APPLICANT: Lagace, Robert, E. APPLICANT: Patterson, Chandra APPLICANT: Patterson, Chandra APPLICANT: Patterson, L. TITLE OF INVENTION: NUCLECTION SEQUENCES OF MORAXELLA CATARRHALIS GENOME FILE REFERENCE: PM-0008-4 US CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 1099-06-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 19988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1287 AATCCAAAAAGGCTTTAAATTTTAATTTCTTTGTTGCATAAAATATCA 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Length 19988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.1%; Score 23; DB 4; Length 1996 68.1%; Pred. No. 65; tive 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No.,6632636 10
PRESICATION INFORMATION:
US-09-596-002-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7, 2004, 15:44:33
                                                                                           Sequence 10, Application US/09596002
Patent No. 6632636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.1
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: M. catarrhalis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 7
Job time: 34.6094 secs
                                               RESULT 15
US-09-596-002-10/c
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Batent No. 6673910
Batent No. 6673910
Batent No. 673910
Batent No. 673910

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT PILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRINCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR PLILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                    263 ATATTAATGAAGTGGACTTAAATGTACGTCCTTTTGTTCTTAAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
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                                                                                                                                                                                                                                                                                        1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAA 44
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                                                                                                                                                                                       Query Match
45.5%; Score 23.2; Di
Best Local Similarity 70.5%; Pred. No. 42;
Matches 31; Conservative 0; Mismatches
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
45.5%; Score 23.2;
Best Local Similarity 77.8%; Pred. No. 43
Matches 28; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1278, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; CRGANISM: Staphylococcus epidermidis
US-09-134-001C-1278
                                                                                         TYPE: DNA; CRGANISM: Acinetobacter baumannii
US-09-328-352-1552
CURRENT FILING DATE: 1999-06-04 WINDER OF SEQ ID NOS: 8252 ERQ ID NO 1552 LENGTH: 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 68.1
Matches 32; Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-1082
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US-09-540-236-1082/c
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Gaps

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(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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- nucleic search, using sw model OM nucleic

May Run on:

7, 2004, 11:56:28 ; Search time 104.189 Seconds (without alignments) 2079.475 Million cell updates/sec

1 acaaaaagaaattggactta......ttttgtgcttcaaacatcat US-10-071-411A-1_COPY_450_500 Perfect score: Sequence: Title:

51

IDENTITY NUC Scoring table:

3373863 seqs, 2124099041 residues Gapop 10.0 , Gapext 1.0

Searched:

6747720 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

N Geneseq 29Jan04:* geneseqn1980s:* genesequ1990s:* geneseqn2000s:* Database :

geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2001as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CTIMMADITE

SUMMARIES	Description	73 Abt11173 Human 5-1	. Abt11114	.6 Abl32116 Human imm	7 Abl32117	7	Abk31176	Ab170132	11 Abl70131 Chemicall		Acc69139	ro.	10-4 Continuation (5 of	ı	Abl33441 Human imm	52 Abl54362 Chemicall	Adc87621 Human GPC	21 Abv58521 Human pro	12 Aak81112 Human imm		Aa141059	70 Abk41870 cDNA enco	37 Adb59537 Connectiv	74 Aac80574 Human sec
SUM	ID	ABT1117	ABT11114	ABL32116	ABL3211	ABK3117	ABK31176	ABL70132	ABL7013	ACA39547	ACC69139	AAT58840	AAT58840	AA183146	ABL3344	ABL54362	ADC8762	ABV5852	AAK81112	AAZ93368	AAL41059	ABK41870	ADB59537	AAC80574
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٥	* Query Match	94.1	94.1	75.3	75.3	75.3	75.3	75.3	75.3	56.1	56.1	56.1	56.1	51.8	50.2	50.2	50.2	49.8	49.4	49.4	49.4	49.4	49.4	49.4
	Score	48	48	38.4	38.4	38.4	38.4	38.4	38.4	28.6	28.6	28.6	28.6	26.4	25.6	25.6	25.6	25.4	25.2	25.2	25.2	25.2	25.2	25.2
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Aak81109 Human imm	Aak81111 Human imm	Aak81110 Human imm	Abl34006 Human imm	Abl17308 Drosophil	Abl33240 Human imm	Continuation (2 of	Acd13446 Human DNA	Aai81019 Human pol	Abk72766 Bacillus	Aav84415 Human sec	Aba83198 Human sec	Ach04699 Novel hum	Acd44509 Human cDN	Abk73006 Bacillus	Aak78949 Human imm	Aad48267 Ehrlichia	Abl33138 Human imm	Aal04782 Human rep	Abl97677 Human tes	Ada02576 Human FKB	Adb72314 Human FKB	
AAK81109	AAK81111	AAK81110	ABL34006	ABL17308	ABL33240	AAL52246 1	ACD13446	AA181019	ABK72766	AAV84415	ABA83198	ACH04699	ACD44509	ABK73006	AAK78949	AAD48267	ABL33138	AAL04782	ABL97677	ADA02576	ADB72314	
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ALIGNMENTS

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Human, polymorphic region, 5-lipoxygenase, 5-LO gene, asthma, bronchitis, simusitis; ulcerative colitis, nephritis; amyloidosis, sarcoidosis, rheumatoid arthritis; scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome; psoriasis; pelvic inflammatory disease, atopic, contact dermatitis, forensic medicine; paternity testing; enzyme;
                                                                     Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
                 BP.
                 ABT11173 standard; DNA; 168174
                                                   (first entry)
                                                                                                                                                                      WO200262825-A2.
                                                                                                                                                      Homo sapiens.
                                                   05-DEC-2002
                                   ABT11173;
RESULT 1
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15-AUG-2002.

07-FEB-2002; 2002WO-US003546.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC.

Meyer J; Barnes G, WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma.

Disclosure; Fig 4; 290pp; English.

The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 20 per pair sequences, given in the specification, or their complement. The compositions and methods of the

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associated with an aberrant inflammatory response such as asthma, bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, posciasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polynuclectide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
present invention are useful for diagnosing and/or prognosing disorders
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Sequence 168174 BP; 46808 A; 36442 C; 36942 G; 46474 T; 0 U; 1508 Other;

ö ö Length 168174; 4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT Indels 94.1%; Score 48; DB 6; Lk 100.0%; Pred. No. 8.9e-06; iive 0; Mismatches 0; Conservative Local Similarity es 48; Conserv Query Match Best Loc Matches

166822 AAAAGAATITGGACTITAAAGTTAATACTTTTGTGCTTCAAACATCAT 166869 qq ð

ABT11114 standard; DNA; 168273 (first entry) 05-DEC-2002 ABT11114; RESULT 2

BP

Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.

Human, polymorphic region, 5-lipoxygenase, 5-LO gene, asthma, bronchitis, sinusitis; ulcerative colitis, nephritis; amyloidosis; sarcoidosis; rheumatoid arthritis; scleroderma; lupus, non-allergic rhinitis; polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;

Homo sapiens.

WO200262825-A2

15-AUG-2002.

07-FEB-2002; 2002WO-US003546.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC.

Meyer J; Barnes G,

WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma

Disclosure; Fig 2; 290pp; English.

comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the present invention are useful for diagnosing and/or prognosing disorders associated with an abstrant inflammatory response such as asthma, bronchitis, sinusitis, ulcerative collitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory The invention relates to an isolated human nucleic acid molecule

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                 also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polynuclectide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvuleant; ophthalmological; antirheumatic; antiartic; antifaibetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                          Sequence 168273 BP; 46834 A; 36467 C; 36966 G; 46498 T; 0 U; 1508 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
disease, atopic and contact dermatitis. The nucleic acid molecules can
                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                            166921 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 166968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
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                                                                                                                                                 Length 168273;
                                                                                                                                                                                                                         4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 89; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 89.
                                                                                                                                                                                    0
                                                                                                                                               DB 6; Le:
8.9e-06;
                                                                                                                                  94.1%; Sco. 100.0%; Pred. No. 0. 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP007537.
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                                                                                                                                                                                    48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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Best Local Similarity
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Matches
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Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                       Signal transduction associated gene modified complementary DNA #10.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 20; 24pp; English.
                                                                                                                                                                                                                     29-JUN-2001; 2001WO-EP007472.
                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
             (first entry)
                                                                                                                                                                                                                                                                                                                  Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                            WPI; 2002-147896/19.
                                                                                                                                                               WO200200926-A2
                                                                                                                        Homo sapiens
             23-APR-2002
                                                                                                                                                                                          03-JAN-2002
                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                        gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                 antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                     system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
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                                       3662 AAAAGAAATTGGATTTAAAGTTAAATATTTTTGTGTTTTAAATATTTTT 3709
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             4 AAAAGAAATIGGACTIAAAGTIAAATACTITIGIGCTICAAACAICAT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38.4; DB 6; Length Logical Pred, No. 0.0082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 90; 32pp + Sequence Listing; German.
                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 90.
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                                                                                                          ABL32117 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP007537
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01-SEP-2000; 2000DE-01043826
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87.5%;
                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piepenbrock
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         WO200200928-A2
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methylation.
                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002.
                                                                                                                                      ABL32117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            olek A,
                                                                                                                                                                                                                     Human;
                                                                                           Matches
                                                                               RESULT 4
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Berlin K;

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signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (pgd islands) of these genes, and a method of or the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell innes, bloopies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó,
The present invention relates to chemically modified DNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.3%; Score 38.4; DB 6; ilarity 87.5%; Pred. No. 0.0082; Conservative 0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Patent Office
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les 42; Conserv
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ABK31177 standard; DNA; 13249 BP.

ABK31177:

ABK31177/c ID ABK311 XX AC ABK311

RESULT 5

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Cell signalling, cytosine methylation, cell signalling disease, cancer, tumour; cytostatic; ds.
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                                                             (EPIG-) EPIGENOMICS AG.
                                                                           WPI; 2002-147896/19
                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 42; Conserv
                            WO200200926-A2.
                                                                                                                                                                                                                                              01-JUL-2002
                  sapiens
                                    03-JAN-2002
                     Synthetic.
                                                                                                                                                                                                                                       ABL70132;
                                                                     olek A,
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The invention relates to a nucleic acid comprising a sequence of at least the bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as a cligonucleotides and/or bNA-oligonurs for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell signalling, cytosine methylation, cell signalling disease, cancer; tumour; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
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Pred. No. 0.0082;
0; Mismatches 6; Indels 0;
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01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 87.5%;
Matches 42; Conservative
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library Library Library Content and Publy sequences are chemically modified using a solution of bigulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or Pub Algomers for detecting the cytosine methylation state (OFG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA, e.g. cell ines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and cherapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequences. Described the printed are sequenced because the disparent did not form part of the printed sequenced at a for this patent did not form part of the printed sequenced.
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                         Human, signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonuclectide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to chemically modified DNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 0.0082;
0; Mismatches (
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01-SEP-2000; 2000DE-01043826.
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Gaps

21

29-JUN-2001; 2001WO-EP007471

30-JUN-2000; 2000DE-01032529

WPI; 2003-029926/02.

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01-SEP-2000; 2000DE-01043826
       (EPIG-) EPIGENOMICS AG
                     WPI; 2002-154758/20
                                                                                                                                                                                           drug design; gene.
                                                                                                                                                                                                        WO200277183-A2.
                                                                                                                                                                                                                03-OCT-2002.
                                                                                                                                                                  ACA39547;
              olek A,
                                                                                                                                                       ACA39547/c
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligoners for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                      Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic
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                                                                                                                                                                                                                                                                                                     with cell signaling e.g. cancer, comprises chemica
sequences of genes associated with cell signaling.
Berlin K;
Piepenbrock C,
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0
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                                                                                                              3662 AAAAGAAATTGGATTTAAAGTTAAATÁTTTTTTGTGTTTTTAAATATTAT 3709
Length 13249;
                                                                            4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                          6; Indels
 Score 38.4; DB 6;
Pred. No. 0.0082;
0; Mismatches 6;
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   Query Match
Best Local Similarity 87.5%;
Matches 42; Conservative
                                                                                                                                                                                                      ACA39547 standard; DNA; 879
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Antisense; ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                   Prokaryotic essential gene #21204.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SET-2001; 2001US-00948993.
25-GCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00372851.
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Trawick JD,
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Wall D,
PRINTER SERVICE SERVIC
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Mycoplasma genitalium.

Zyskind JW; Xu HH;

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the intraction relates given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mocleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the proliferation or the activity of a gene in an operan required for proliferation or the activity of a gene in an operan required for the gene product or that has an activity against a biological pathway required for cellular proliferation or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolifing a compound's activity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibiotic; (10) prolifing a compound's activity; (11) a culture comprising strains in which the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying proteins or soreening for homologous nucleic acids required for collular proliferation to solare andidate molecules for racional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, F. premoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from vint/pub/published_pot_sequences
                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid comprising any one of
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56.1%; Score 28.6; DB 7; Length 879;
Best Local Similarity 72.5%; Pred. No. 8.8;
Matches 37; Conservative 0; Mismatches 14; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 879 BP; 269 A; 120 C; 143 G; 347 T; 0 U; 0 Other;
                                                                                                                                                                                                                         Claim 14; SEQ ID NO 27417; 1766pp; English.
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                                                       P-PSDB; ABU35677
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AAT58840 4
Continuation (5 of 6) o
WP Sequence split into
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                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                             RESULT 13
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Continuation (6 of 6) of AATS8840 from base 500001 (Mycoplasma genitalium genome.
WP Sequence split into 6 fragments LOCUS AATS8840 Accession Aat58840
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                                                                                                                                                                                                                                                                             The present invention describes a basic genetic operating system for an autonomous prototrophic or auxotrophic nanomachine comprising a minimal gene set sufficient for viability or replication, optionally in the presence of an auxotrophic molecule. Also described is an autonomous prototrophic or auxotrophic molecule. Accomprising a basic genetic operating system for autonomous prototrophic or auxotrophic molecule, and a particle envelope. The nanomachines can be used in gene therapy. The basic genetic operating system or nanomachine is useful in therapeutic, diagnostic and industrial applications, e.g. as bioreactor, for bioremediation, for the production of a therapeutic biomolecule or as a therapeutic reagent, for the production of a diagnostic indicator or reagent, as a delivery system, as an artificial diagnostic indicator or reagent, as a delivery system, as an artificial
                                                                                                                                                                                   New basic genetic operating system for autonomous prototrophic or auxotrophic nanomachine, useful for therapeutic, diagnostic or industrial purposes, comprises a nanomachine genome encoding a gene set for viability or replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue or organ system, as an energy conversion system, as a processing system, as an anabolic or catabolic system, for the production of biological films or coatings, and for cosmetic applications. The present sequence represents a Mycoplasma genitalium gene cassette nucleotide sequence, which is used in an example from the present invention for the design and synthesis of a basic genetic operation system for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
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Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                         Example 1; Page 210-213; 250pp; English
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410000
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580073
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Best Local Similarity 72.5%;
Matches 37; Conservative
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200001
300001
400001
500001
                                                    18-SEP-2002; 2002WO-US029811.
                                                                             20-SEP-2001; 2001US-00960870
                                                                                                         (EGEA-) EGEA BIOSCIENCES INC
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Matches 37; Conservative
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WO2003025145-A2
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AAT58840 1
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AAT58840 3
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                           27-MAR-2003
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AAT58840 from base 400001 (Mycoplasma genitalium genome. ) fragments LOCUS AAT58840 Accession Aat58840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cytokine; cell proliferation; cell differentiation, gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                   LOCUS AAT58840 Accession Aat58840
End
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Pred. No. 12;
0; Mismatches
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310000
410000
510000
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18-MAY-2000; 2000US-00577409
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72.5%;
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400001
500001
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                   9 of
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37; Conserva
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                                                                                                          Fragment Name
AAT58840 0
AAT58840 1
AAT58840 2
AAT58840 3
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AAT58840 5
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebuxaemia, Alzhaimer's disease, Alzhailepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful idiagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system disease; cytosine methylation; antiasthmatic;
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                                                                   Length 355;
                                                                                                                                                                                                                                                           209 ATAAATTGGACTTAAAATTCAAAACTCTTGCCCTTTAAAAGACA 166
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                                                                                                                                          Indels
                                                                                                                                                                                                              7 AGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA 50
Sequence 355 BP; 86 A; 65 C; 74 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 1414.
                                                                                                                                      11;
                                                                       DB 4;
                                                               51.8%; Score 26.4; D
75.0%; Pred. No. 41;
tive 0; Mismatches
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                              Conservative
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                                                                                                            Local Similarity
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                                                                       Query Match
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ABEJ33441/C
ID ABEJ3
XX
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ABEJ3
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DE Human
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MW Human
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This invention relates to chemically pre-treated DNA of genes associated with apoptosis. The mucleic acids are used to allocate patients for specific therapy for HIV infection, Bloom syndrome, cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours and cancers. This nucleotide sequence represents a chemically treated apoptosis gene. Even SEQ ID numbers are the complementary DNA strands to the odd SEQ ID numbers. The sequence data for this patent is not represented in the printed specification but is based on information supplied by the
                                                                                                                                                         syndrome, cardiopathy, neurodegenerative disorder, renal ischaemia, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
                                                                                                                            Chemically treated apoptosis gene complementary to gene #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACAT
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70.8%; Pred. No. 89;
tive 0; Mismatches
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07-APR-2000; 2000DE-01019173.
30-UUN-2000; 2000DE-01035529.
01-SEP-2000; 2000DE-01043826.
                              ABL54362 standard; DNA; 5864
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                                                                                              entry)
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Matches 34; Conservative
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Search

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Gaps

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DB 6; Length 5864;

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Query Match Best Local Similarity

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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33 33 36 36 37 38 38 40 40 40 40 40 40 40 40 40 40 40 40 40	9 143878	AL359974	AL3599/4 Homo sapi
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		ALIGNMENTS	
RESULT 1			
;		129266 bp DNA	linear PRI 20-JUN-2002
DEFINITION Human DNA	DNA sequence	Irom clone KFII	CITCOMOSOME TO
sednence.	Ge.		

AL731567	
LOCUS	AL731567 129266 bp DNA linear PRI 20-JUN-2002
DEFINITION	Human DNA sequence from clone RPII-67C2 on chromosome 10, complete
	sequence.
ACCESSION	AL731567 AC010865
VERSION	AL731567.6 GI:21537524
KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 129266)
AUTHORS	Whitehead, S.
TITLE	Direct Submission

JOURNAL

COMMENT

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Perreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Mowland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lecke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M., Wheeler,J., Mu,X.,
Direct Submission
                                                                                                                                                                                                                                                                                            Submitted (15-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 14, 2000 this sequence version replaced gi:6524208.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 16_P 14

Sequencing vector: M13, M79815; 100% of reads
Sequencing vector: M13, M79815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 111055 bases at least Q40
Consensus quality: 115066 bases at least Q30
Consensus quality: 147921 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 157754; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
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gap of 100 bp
contig of 1509 bp in length
gap of 100 bp
gap of 100 bp
contig of 1209 bp in length
gap of 100 bp
contig of 1551 bp in length
gap of 100 bp
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gap of 100 bp
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of 1143 bp in length
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contig of 1641 bp in length
gap of 100 bp
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of 2712 bp in length
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                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                  http://www.genomecorp.com
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSRROT; Tr., TREMBL; WD:, WORMERP; Information mis conditions of the WORMERP.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Bandwin,J., Barna,N., Beckerly,R., Bouslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Collangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPII-67C2 is from the library RPCI-11.1 constructed by the group of Pieter de Jong, For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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1 (Dases 1 to 160654)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, Conne RP11-16P14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
                   Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
                                         Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:21213582.
Draft Sequence Produced by Genome Therapeutics Corp, 100 Beaver
Street, Waltham, MA 02453, USA
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Pred. No. 0.00039;
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100.0%; Pred. No. v...
0; Mismatches
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'mol type="genomic DNA"
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/clone_lib="RPCI-11.1"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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FEATURES

DEFINITION

RESULT 2 AC011879 LOCUS

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ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS JOURNAL REFERENCE

TITLE

AUTHORS

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194453 bp DNA linear HTG 30-AUG-2001
Homo sapiens chromosome 06 clone RP11-326D18, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
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Submitted (25-SEP-1999) Genome Therapeutics Corporation, 100 Beaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: hg024
------ Summary Statistics
Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
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On Sep 1, 2000 this sequence version replaced gi:8247773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40267 AAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 40314
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Center code: GTC
Web Site: http://www.genomecorp.com/
Contact: gtc-segcenter@genomecorp.com
Project Information
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AC010862.7 GI:9957987
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
Homo sapiens
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83766..95322
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36727. .42109
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42210. .48339
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74044. .83665
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133059. .145697
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                              55434. 63594 '-
/note="assembly_fragment"
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3: contig of 10249 bp in length
3: gap of 100 bp
5: contig of 9622 bp in length
6: gap of 100 bp
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g of 11557 bp in length
f 100 bp
g of 12981 bp in length
1: contig of 1770 bp in length gap of 100 bp in length is contig of 2682 bp in length is gap of 100 bp in length is contig of 5028 bp in length is gap of 100 bp in contig of 5383 bp in length is contig of 5383 bp in length is gap of 100 bp in contig of 6894 bp in length is gap of 100 bp in length in length in gap of 100 bp in length in length in gap of 100 bp in length in l
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of 8161 bp in length
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1. .151
/note="assembly_fragment
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/note="assembly_fragment"
25642. .28323
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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8183. .20523
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note="assembly_fragment"
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rector_side:right"
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vector_side:right"
252. .1760
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Assembly program: Phrap; version 990315
Consensus quality: 162991 bases at least Q40
Consensus quality: 176452 bases at least Q30
Consensus quality: 178970 bases at least Q20
Insert size: 122053; sum-of-contigs
Quality coverage: 4.2x in Q20 bases; sum-of-contigs
                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 2s contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the agas are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Location/Qualifiers
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157299: gap of unknown length
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of 2253 bp in length
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1217; gap of unknown length
2365: contig of 1148 bp in length
2465: gap of unknown length
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/db_xref="taxon:9606"
/db_cxosome="06"
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/clone_lib="RPCI-11"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 20 03-JAN-2002;
Epigenomics AG (DE)
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 19 03-JAN-2002;
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94.1%; Score 48; DB 2; Lv
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ive 0; Mismatches 0;
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Sequence 19 from Patent WO0200926.
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Location/Qualifiers
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ALS90439 192044 bp DNA linear PRI 23-AUG-2001
Human DNA sequence from clone RPI1-394I23 on chromosome 10,
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1 (bases 1 to 192044)
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Submitted (23-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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/mol_type="unassigned DNA"
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/noTe="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                     Location/Qualifiers
1. .13249
/organism="synthetic construct"
/organism="synthetic DNA"
/mol type="unassigned DNA"
/db xref="texon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with cell signalling
Patent: WO 0202807-A 22 10-JAN-2002;
                                                   Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with cell signalling Patent: WO 0202807-A 21 10-JAN-2002; Epigenomics AG (DE)
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llarity 87.5%; Pred. No. 0.33;
Conservative 0; Mismatches
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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1. 13249
Acranism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"
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Sequence 21 from Patent WO0202807.
AX348563
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Sequence 90 from Patent WO0200928.
AX345019
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Sequence 89 from Patent WO0200928.
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Consensus quality: 116698 bases at least Q40
Consensus quality: 124565 bases at least Q30
Consensus quality: 125980 bases at least Q30
Consensus quality: 125980 bases at least Q30
Consensus quality: 125980 bases at least Q30
Estimated insert size: 130000; pulse field gel estimation
Estimated insert size: 130000; pulse field gel estimation
Quality coverage: 4.18 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 16 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be reserved.

* This sequence will be preserved.

* $17912 contig of $175 bp in length

* $1792 contig of $175 bp in length

* $2227 22476: contig of $15278 bp in length

* $25477 25576: gap of unknown length

* $2577 25576: gap of unknown length

* $5090 52189: gap of unknown length

* $5000 52189: gap of unknown length

* $5000 52189: gap of unknown length
Submitted (14-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7711854.
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/clone_lib="CalTech human BAC library D"
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Center clone name: CITB-H1_2235A13
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/organism="Homo sapiens"
                                                                                                          -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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chromosome="5"
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                                                                              COMMENT
requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14268248.
During sequence assembly data is compared from overlapping clones.
Mere differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the voratation amnotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSEROT; Tr.; TREMBL; WORMPEP; Information on the WORMPEP database can be found a attention on the minimal database.
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The true right end of clone RPII-394123 is at 192044 in this sequence. The true left end of clone RPII-657A9 is at 85254 in this sequence. The true left end of clone RPII-657A9 is at 100 in this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11.394123 is from the library RPCI-11.2 constructed by the group of Pleter de Jong. For further details see
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128529)
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VECTOR: pBACe3.6
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Sequencing of Human Chromosome 5
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/clone="RP11-394I23"
/clone_lib="RPCI-11.2"
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HTG; HTGS PHASE2; HTGS DRAFT.
Homo sapiens (human)
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Submitted (16-MAY-2003) Shih-Feng Tsai, National Health Research Institutes (NHRI), Division of Molecular and Genomic Medicine; 128, Yen-Chiu-Yuan Road, Sec 2, Taipel 115, Taiwan
Yen-Chiu-Yuan Road, Sec 2, Taipel 115, Taiwan
Tel:886-2-28267313, Fax:886-2-28200552)
The Chimpanzee Chromosome 22 Sequencing Consortium consists of: "Chimpanzee Chromosome 22 Sequencing Consortium consists of: "Chimpanzee National Human Genome Center at Shanghai, Shanghai, China; "CBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
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                                                                                                                                                                                                                                                         Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
1 (bases 1 to 164217)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164217)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edm
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
Location/Qualifiers
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Homo sapiens (human)
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-JUN-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 28, 2003 this sequence version replaced gi:14993661. Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (26-JUN-2001) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
1 (bases 1 to 157325)
DOB Joint Genome Institute and Stanford Human Genome Center.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens chromosome 5 clone CTD-2096123, complete sequence
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Quality: Phrap Quality >=40 99.7% of Sec
Estimated Total Number of Errors is 0.3.
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/mol_type="genomic DNA"
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DOE Joint Genome Institute.
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Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
ORGANISM
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REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

ACCESSION VERSION

KEYWORDS

RESULT 13

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AC093264

0

Gaps

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Gaps

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Length 209016;

ROD 29-JUN-2002

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Diract Submission

Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquaries:

Rumbridgeshire, CB10 18A, UK. E-mail enquaries:

Rummridgeshire, CB10 18A, UK. E-mail enquaries:

Running sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MIS subclone; and the assembly was contirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP; Harming on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                             AL365334 173053 bp DNA linear ROD 29-JUN-2002
Mouse DNA sequence from clone RP23-392F1 on chromosome 1, complete
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 173053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-392Fl is from the RPCI-23 Mouse PAC Library—constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
                                                                                                                                                                                                                                 1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ser code: UK-MRC
site: http://mrcseq.har.mrc.ac.uk
                                                                                             Score 33.4; Di
Pred. No. 3.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32.6; DE
Pred. No. 6.6;
0; Mismatches
                'note="low quality region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ Genome Center
Center: UK Medical Research Council
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://mrcseg.har.mr
Contact: mouseg@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP23-392F1"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:20068419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                          65.5%;
ilarity 78.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.9
Best Local Similarity 80.9
Matches 38; Conservative
                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL365334
AL365334.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blakey, S
                                                                                                                                               40;
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                            RESULT 15
AL365334/c
                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                         ORIGIN
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                                                                                                                                                                                                   ò
                                                                                                                                                    Center: National Yang Ming University Genome Research Center Center
                                                                                                                                                                                                                                                             PTB1 Chimpanzee BAC library was prepared from DNA isolated from ltured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were double stranded, sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Quality Assessment:
This entry has been annotated with sequence estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                          Sequencing vector: DVC18; 100% of reads
Sequencing vector: DVC18; 100% of reads
Chemistry: DVG-terminator Big Dye and ET; 100% of reads Assembly
program: Phrap; version 0.990319
Consensus quality: 207,750 bases at least Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="gap containing unresolved di-nucleotide repeats,
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany, *National Institute of Genetics, Mishima, Japan; *National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neighboring clones: PTB-152N20(left) and RP43-055A16(right) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and the assembly was confirmed by restriction digest.
                                                                                                        *RIKEN Genomic Sciences Center, Yokohama, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chronosome="22"
/clone="PTB-153E07"
/clone="PTB-15E07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subclone or more than one M13 subclone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16459. ..16463
/note="low quality region"
43909. .44908
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6277. .46280
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128691
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                                                                                                                                                                                                              Web site: http://genome.ym.edu.tw/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.gsc.riken.go.jp).
VECTOR: pKS145
                                                                                                                                         Genome Center
                                                                                                                                                                                                                                            Contact: sequence@ym.edu.tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .45771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45769.
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                                                                                                                                                                                     code: YMGC
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Gaps

Indels

Length 173053;

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Search completed: May 7, 2004, 14:30:58 Job time : 538.003 secs

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Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1069, Ap
Sequence 1069, Ap
Sequence 1, Appli
Sequence 690, Appli
Sequence 690, Appli
Sequence 690, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1082, Apple Sequence 10, Appl Sequence 30, Appl Sequence 1, Appli Sequence 172, Appli S
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1038, Ap
1118, Ap
2188, Ap
1, Appli
                                                                                                                                                7, 2004, 13:35:03 ; Search time 25.6094 Seconds (without alignments) 1105.159 Million cell updates/sec
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Sequence 1278, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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(GGDZ_6/ptodata/2/ina/5A_COMB.seq:*

(GGDZ_6/ptodata/2/ina/5B_COMB.seq:*

(GGDZ_6/ptodata/2/ina/6A_COMB.seq:*

(GGDZ_6/ptodata/2/ina/6B_COMB.seq:*

(GGDZ_6/ptodata/2/ina/PCTUS_COMB.seq:*

(GGDZ_6/ptodata/2/ina/PCTUS_COMB.seq:*

(GGDZ_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-67-258-15

US-08-680A-3

US-08-8175-3

US-08-476-891A-3

US-08-476-891A-3

US-09-976-594-1669

US-09-976-594-1669

US-09-976-594-690

US-09-976-594-690

US-09-976-594-690

US-09-976-594-690

US-09-976-594-690

US-09-976-594-690

US-09-976-594-690

US-09-134-001C-1278

US-09-596-002-10

US-09-596-002-10

US-09-596-002-10

US-08-956-171E-530

US-08-956-171E-530
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US-09-134-001C-1118
US-09-328-352-2188
US-08-956-171E-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                            682709 segs, 277475446 residues
                                                                                                                                                                                                                                              US-10-071-411A-1_COPY_450_500
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Maximum Match 99%
Listing first 45 summaries
                                                                                                   - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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48.2 1018
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Sequence 1, Application US/08545528D

Patent No. 653773

GENERAL INFORMATION:

APPLICANT: Fraser et al.

TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragme;

FILE REFERENCE: P8193P1

TITLE OF INVENTION: Thereof, and Uses Thereof

FILE REFERENCE: P8193P1

CURRENT PILING DATE: 1995-10-19

PRIOR APPLICATION NUMBER: US 08/488,018

PRIOR APPLICATION NUMBER: US 08/473,545

PRIOR APPLICATION NUMBER: US 08/473,545

FRIOR PILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 1

SEQ ID NO 1

LENGTH: 580073
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               Sequence 2724, App
Sequence 3265, Ap
Sequence 1305, Ap
Sequence 29, Appli
Sequence 6, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 15, Appli
                                                                                                       17, Appl
15, Appl
14, Appl
3, Appli
2161, Ap
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Sequence 150, App
                                                                                                                                                                                                                        3, Appl:
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                                                                                                                                    Sequence 1
Sequence 3
Sequence 2
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Sequence
Sequence
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                                                     US-09-800-729-29
US-09-380-729-29
US-09-388-383C-4
US-09-358-383C-17
US-09-358-383C-17
US-09-358-383C-14
US-09-358-383C-14
US-09-734-674-3
US-09-734-674-3
US-09-734-674-3
US-09-734-674-3
US-09-134-001C-65
US-09-21-017B-113
US-08-714-168-3
US-09-320-721A-3
US-08-961-527-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PS007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,885
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER FILING NUMBER: 60/049,375
EARLIER FILING NUMBER: 60/049,881
               US-09-134-001C-2724
US-09-543-681A-3265
US-09-134-000C-1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
            813 4
1245 4
1281 4
1628 2
2694 2
3321 5955
202001
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904
1044
11137
1782
1782
5238
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RESULT 2
US-09-205-258-15
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                                                                                                                                                              Query Match
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BARLIER FILING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/048, 991

BARLIER PILING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/048, 991

BARLIER APPLICATION NUMBER: 60/048, 992

BARLIER APPLICATION NUMBER: 60/048, 993

BARLIER APPLICATION NUMBER: 60/048, 993

BARLIER PILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/048, 915

BARLIER APPLICATION NUMBER: 60/048, 915

BARLIER FILING DATE: 1997-06-06

BARLIER FI
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Sequence 3, Application US/08567375

Patent No. 595246

GENERAL INFORMATION:

APPLICANT: Ronald, Pamela C.

APPLICANT: Sanbo, Veronique

TITLE OF INVENTION: Disease Resistance in Plants

MUMBER OF ENQUENCES:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

STREET: Two Embarcadero Center, Eighth Floor

GITY: San Francisco

GONFUTER: EIM PC Compatible

COMPUTER: EIM PC Compatible

MEDIUM TYPE: Ploppy disk

COMPUTER: EIM PC Compatible

COMPUTER: ENDARE: PLOPS/MS-DOS

OFFRATION STREE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US 60/004,645

FILING DATE: 10-289-1995

RING APPLICATION DATH:

APPLICATION NUMBER: US 08/373,375

FILING DATE: 17-3N-1995

ATTORNEY AGENT INFORMATION:

REPERENCE/DOCKET NUMBER: US 08/373,375

FILING DATE: 17-3N-1995

ATTORNEY AGENT INFORMATION:

REPERENCE/DOCKET NUMBER: 34,774

REPERENCE/DOCKET NUMBER: 36,774

TELECHOMUTICATION POR 23

SEQUENCE GERAACTERISTICS:

FROUNCE SERVICES.

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FROUNCE SERVICES.

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                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                    Query Match 48.2%; Score 24.6; DB 4; I
Best Local Similarity 70.2%; Pred. No. 15;
Matches 33; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | NAME/KEY: CDS | LOCATION: join(1..2676, 3520..3918) | COCATION: join(1..2676, 3520..3918) | US-08-567-375-3 | LOCATION: /product= "Xa-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3921 base pairs
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 1018
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STRANDEDNESS: single
                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-09-205-258-15
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US-08-567-375-3/c
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RESULT 5

US-08-475-891A-3/C

Sequence 3, Application US/08475891A

Patent No. 585939

GENERAL INFORMATION:

APPLICANT: Ronald, Pamela C.

APPLICANT: Ronald, Pamela C.

APPLICANT: Ronald, Penela C.

APPLICANT: Ronald, Penela C.

APPLICANT: Bong, Wen-Yuang

TITLE OF INVENTION: Disease Resistance in Plants

NUMBER OF SEQUENCES: 15

CORRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

TITLE OF INVENTION: Disease Resistance in Plants

NUMBER OF SEQUENCES: 15

CORRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STREET: Two Embarcadero Center, Eighth Floor

STREET: Two Embarcadero Center, Eighth Floor

CONFUTER: Elby PC Compatible

COMPUTER: Elby PC Compatible

COMPUTER: READABLE FORM:

MEDIUM TYPE: RIP PC Compatible

COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/373,375

FILING DATE: 17-JAN-1995

CLASSIFICATION NUMBER: US 08/373,375

FILING DATE: 17-JAN-1995

MATCRIEY APPLICATION NUMBER: US 08/373,375

FILING DATE: TAMENDATION:

NAME: Bastian, Kevin I.

REGISTRALION NUMBER: 24,774

REBERRANCE/DOCKET NUMBER: 27,000-058910US

TELECOWUNINICATION NUMBER: 27,000-058910US
                                                                 3456 Araaaakdaaciriddargiaraarrargiaaairiacdrgiraaaraica 3407
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CTHER INFORMATION: /product= "RRK-B"
CTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-B from rice (Oryza US-08-475-891A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 52, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.0
Matches 34; Conservative
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STRANDEDNESS: sing
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                                                              Gaps
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Query Match
47.8%; Score 24.4; DB 2; Length 3921;
Best Local Similarity 68.0%; Pred. No. 19;
Matches 34; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
APPLICANT: Szabo, Veronique
APPLICANT: Szabo, Transis for Conferring
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3921;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
SOFTWARE: FREEHINE RELEASE #1.0, Version #1.30
SOFTWARE: FREEHIN Release #1.0, Version #1.30
SOFTWARE: PRECRICATION DATA:
RPPLICATION NUMBER: US/08/587,680A
RILNG APPLICATION DATA:
RPPLICATION DATA:
RPPLICATION DATA:
RPPLICATION DATA:
RPPLICATION DATA:
RPPLICATION NUMBER: US 08/475,891
FILING DATE: US-SEP-1995
RILOR APPLICATION DATA:
RPPLICATION NUMBER: US 08/567,375
FILING DATE: US-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BASELIAH, Kevin L.
RRGISTRALION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058940US
TELECOMMUNICATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: O23070-058940US
TELECOMMUNICATION INFORMATION:
THEREPARENCE/DOCKET NUMBER: O23070-058940US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
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68.0%; Pred. No. 19;
iive 0; Mismatches 16;
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; OTHER INFORMATION: /product= "Xa-21"
US-08-587-680A-3
                                                                                                                                                                                                                                  RESULT 4
US-08-587-680A-3/c
'Sequence 3, Application US/08587680A
'PALENT NO. 5977434
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEBERX: (415) 576-0200
TELERX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER.STICS:
LENGTH: 3921 harr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear |
MOLECULE TYPE: DNA (genomic)
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 34; Conserv
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Gaps

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PAPLICANT: Young et al.
TITLE OF INDRATION. 207 Human Secreted Proteins FILES APPLICATION WUMBER: US/09/205,258
CURRENT FILING DATE: 1938-12-04
EARLIER FILING DATE: 1938-06-04
EARLIER FILING DATE: 1937-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER PLING DATE: 1997-06-06
EARLIER APPLICATION WUMBER: 60/048,096
EARLIER FILING DATE: 1997-06-06
EARLIER PLING DATE: 1997-06-06
EARLIER APPLICATION WUMBER: 60/048,096
EARLIER PLING DATE: 1997-06-06
EARLIER APPLICATION WUMBER: 60/048,096
EARLIER PLING DATE: 1997-06-06
EARLIER APPLICATION WUMBER: 60/048,096
EARLIER APPLICATION WUMBER: 60/048,096
EARLIER PLING DATE: 1997-06-06
EARLI
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDE
FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PELLING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6673549 107309.1

NAME/KEY: unsure

LOCATION: 433-436, 445, 447, 454, 456, 463-465, 472, 495, 498, 662, 939

OTHER INFORMATION: a, t, c, g, or other

US-09-976-594-1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 4; Length 1856;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 CAAAAAGATAGAGGATTTAAATTTCACAATTGATGTGCTTTAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.8;
Pred. No. 27;
                                                          EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PELING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/02,921
EARLIER APPLICATION TOWNER: 60/02,921
EARLIER PILING DATE: 1998-07-15
EARLIER PELING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO 52
LENGTH: 1856
                      FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1069, Application US/09976594
Patent No. 6673549
PERERAL INFORMATION:
APPLICANT: Furness, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-976-594-886/c
; Sequence 886, Application US/09976594
; Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.7%;
72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                ch 47.1%;
1 Similarity 68.8%;
33; Conservative (
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.1
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1011
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-976-594-1069
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OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc_feature.
LOCATION: (557203)...(557203)
OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc_feature.
LOCATION: (574435)...(674435)
OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc_feature.
LOCATION: (682442)...(682442)
OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc_feature.
LOCATION: (71352)...(713652)
OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc_feature.
LOCATION: (713552)...(713652)
                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (163385). (163385)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (191989). (191989)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (191995). (191995)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (231980). (231980)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (231980). (231980)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (234187). (234187)
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LOCATION: (312877). (312837)
CTHER INPORATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (312937). (312933)
CTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (319226). (319226)
COTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (559167). (559167)
COTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (559241). (559241)
NAME/KEY: misc feature
LOCATION: (559241). (559241)
NAME/KEY: misc feature
LOCATION: (559241). (559241)
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t
                                                                                                      LOCATION: (103998)...(103998)
OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature
LOCATION: (148948)...(148948)
OTHER INFORMATION: n equals a,
                                 COCATION: (98343) .. (98343)

OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (234220) ... (234220)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
                                                                                  NAME/KEY: misc_feature
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Fatent No. 6503729

GENERAL INFORMATION:

APPLICAMY: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729

TITLE OF INVENTION: jannaschii

FILE REFERENCE: PB275

CURRENT APPLICATION NUMBER: US/08/916,421B

CURRENT FILING DATE: 1997-08-22

FRIOR APPLICATION NUMBER: US 60/024,428

FRIOR APPLICATION NUMBER: US 60/024,428

FRIOR APPLICATION NUMBER: US 60/024,428

NUMBER: OF SEQ ID NOS: 3

SOFTWARE: PATENTIN Version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1218 AAAGAGAAATTTTACATATAGTTAAATAATTTTT 1184
                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 981037.1
US-09-976-594-886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AAAAAGAAATTGGACTTAAAGTTAAATACTTTTGT 37
FILE REFERENCE: PA-0041 US
CURRENT PEPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
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LOCATION: (28257)..(28258)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc feature
LOCATION: (28222) ..(28222)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                      SEQ ID NO 886
LENGTH: 1312
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US-08-916-421B-1
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDE
PILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PLING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 690
LENGTH: 6609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09751389

Patent No. 6630334

GENERAL INFORMATION:

APPLICANT: GUEGIER, Karl et al

APPLICANT: GUEGIER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT PILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 786431

TYPE: DNA

ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.9%; Score 23.4; DB 4; Length 6609; Best Local Similarity 67.3%; Pred. No. 43; Matches 33; Conservative 0; Mismatches 16; Indels 0
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                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No. 6673549 175918.15
NAME/KEY: unsure
COCATION: 825
OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-690
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81.8%; Pred. No. 65
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LOCATION: (1)...(786431)
OTHER INFORMATION: n = A,T,C or G
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Matches 27; Conservative
                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-751-389-3/c
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                                   NAME/KEY: misc_feature
LOCATION: (779455).
OTHER INFORMATION: n equals a, t, c,
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c,
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
  LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1130881). (1130881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1310988).
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (131324). (131324)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1349473). (1349473)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1349491). (1349491)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (147091). (147091)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (14509020)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1569020)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1569020)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1096846)..(1096846)
OTHER INPORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n equals a,
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                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHEK INFORM
US-08-916-421B-1
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Sequence 1552, Application US/09328352
Facent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: BACKER ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BACKMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
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                                                                                       658324 TGAAACTTAAAAACTTTTGTGCCTCAAAAAAA 658292
                                                                                                                                                                      RESULT 12
US-09-328-352-1552
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Gaps

17; Indels

21 0

555193 AAAAAGAAAATTAATCATGCAAATATATATATTTAATGCATCAAACATTAT 555243

Sequence 690, Application US/09976594; Patent No. 6673549; GENERAL INFORMATION:

RESULT 10 US-09-976-594-690/c

g à

1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT

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APPLICANT: Lagace, Robert, E.
APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLECTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1287 AATCCAAAAAGGCTTTAATTTTAATTTCTTTGTTGCATAAATATCA 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.1%; Score 23; DB 4; Length 19988; 68.1%; Pred. No. 65; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No. 6632636 10
; PUBLCATION INFORMATION:
US-09-596-002-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7, 2004, 15:44:33
                                                                                                     Sequence 10, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 19988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 68.1'
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 7
Job time: 34.6094 secs
                                                                                  JS-09-596-002-10/c
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i Sequence 1278, Application US/09134001C

j Patent No. 6380370

general information:
TITLE OF INVENTION:
TITLE OF INVENTION: BPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-06-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 1278
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US-09-540-236-1082/c

Sequence 1082, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:

APPLICAMY: GATY L. Breton et al.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840
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                                                                                                                                                                                            DB 4; Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AATCCAAAAAGGCTTTAAATTTAATTTCTTTGTTGCATAAATATCA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.1%; Score 23; DB 4; Length 1026; Best Local Similarity 68.1%; Pred. No. 49; Matches 32; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                             263 ATATTAATGAAGTGGACTTAAATGTACGTCCTTTTGTTCTTAAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                        13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1360 CAAAAAGAAACTGGTATTAAAGGTAAACAATTATT 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGT 37
                                                                                                                                                                                          Score 23.2; D
Pred. No. 42;
0; Mismatches
                                                                                                                                                                                                                                                                                 1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                              ; TYPE: DNA; CRGANISM: Acinetobacter baumannii
US-09-328-352-1552
CURRENT FILING DATE: 1999-06-04 WIMPER OF SEQ ID NOS: 8252 LENGTH: 963
                                                                                                                                                                                          45.5%;
                                                                                                                                                                                                                                      31; Conservative
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ORGANISM: M.catarrhalis
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-001C-1278
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Gaps

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5.1.6
Compugen Ltd.
 GenCore version (c) 1993 - 2004
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using sw model - nucleic search, OM nucleic

Run on:

7, 2004, 11:56:28; Search time 104.189 Seconds (without alignments) 2079.475 Million cell updates/sec

US-10-071-411A-1_COPY_450_500 Title:

1 acaaaaagaaattggactta.......ttttgtgcttcaaacatcat 51 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

6747720

Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries

geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2003bs:* N_Geneseq_29Jan04:* genesegn1980s:* genesegn1990s:* genesegn2000s:* geneseqn2002s:* 2 4 4 70 6 7 8 9 4 4 0 0 0 1 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:*

geneseqn2004s:*

STIMMARTES

			o\f			SOMMAKIES	
Result No.	ult No.	Score	Query	Length	DB	ID	Description
	-	48	94.1	168174	9	ABT11173	Abt11173 Human 5-1
	7	48	94.1	168273	9	ABT11114	Human 5
	m	38.4	75.3	13249	9	ABL32116	Human
U	4	38.4	75.3	13249	9	ABL32117	Human
υ	Ŋ	38.4	75.3	13249	9	ABK31177	_
	w	38.4	75.3	13249	9	ABK31176	Abk31176 Signal tr
υ	7	38.4	75.3	13249	9	ABL70132	N
	œ	38.4	75.3	13249	9	ABL70131	
υ	σ	28.6	56.1	879	7	ACA39547	-
r U	10	28.6	56.1	10809	^	ACC69139	
	11	28.6	56.1	80073	~		Continuation (6 of
, 1	12	28.6	56.1	110000	~	AAT58840 4	Continuation (5 of
υ	13	26.4	51.8	355	4	AAI83146	r r
Ö	14	25.6	50.2	5864	ø	ABL33441	Human
U	15	25.6		5864	ø	ABL54362	
U	16	25.6		349	σ	ADC87621	
	17	25.4		607	Ŋ	ABV58521	Human
	18	25.2		206	4	AAK81112	
υ	13	25.2	49.4	1214	ო	AAZ93368	Aaz93368 Sequence
	20	25.2	49.4		Ø	AAL41059	Aal41059 cDNA of H
	27	25.2	49.4	1285	4	ABK41870	Abk41870 cDNA enco
U	22	25.2	49.4		ω	ADB59537	7 Conne
. •	23	25.2	49.4	1779	'n	AAC80574	Aac80574 Human sec

Aak81109 Human imm Aak81111 Human imm Aak81110 Human imm	Abl17308 Drosophil	Abl33240 Human imm	Continuation (2 of Acd13446 Human DNA		Abk72766 Bacillus	Aav84415 Human sec	Aba83198 Human sec	Ach04699 Novel hum	Acd44509 Human cDN	Abk73006 Bacillus	Aak78949 Human imm	Aad48267 Ehrlichia	Abl33138 Human imm	Aal04782 Human rep	Abl97677 Human tes	Ada02576 Human FKB	Adb72314 Human FKB
AAK81109 AAK81111 AAK81110	ABL34006 ABL17308	ABL33240	AAL52246_1 ACD13446_	AAI81019	ABK72766	AAV84415	ABA83198	ACH04699	ACD44509	ABK73006	AAK78949	AAD48267	ABL33138	AAL04782	ABL97677	ADA02576	ADB72314
4 4 4	6 4	91	- 1	4	9	~	4	œ	æ	9	4	9	ø	4	4	œ	σ
5728 5733 5733	18434	9888	240000		948	1018	1018	1018	1018	_	3982	4460	5678	22927	22927	87878	87878
4.4.4	49.4	49.0	49.0	48.2	48.2	48.2	48.2	.2	48.2	8.2	.2	48.2	.2	2.2	8.2	.2	8.2
4 4 4 0 0 0	4 4	4	4 4	4	4	4	4	4	4	4	4	4	4	4	48	4	4
25.2 25.2 25.2	25.2	25	5 2 2 2	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6
22 25 26	27	52	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45
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ALIGNMENTS

Human; polymorphic region; 5-lipoxygenase; 5-LO gene; asthma; bronchitis; sinusitis; ulcerative colitis; nephritis; amyloidosis; sarcoidosis; rheumatoid arthritis; scleroderma; lupus; non-allergic rhinitis; polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme; Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63. ABT11173 standard; DNA; 168174 BP (first entry) 05-DEC-2002 ABT11173; RESULT 1 ABT11173

Homo sapiens.

WO200262825-A2.

15-AUG-2002.

07-FEB-2002; 2002WO-US003546.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC.

Meyer J; Barnes G,

WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a belymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as aethma

Disclosure, Fig 4; 290pp; English.

The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-L0) gene, where the allelic variant comprises one or more nuclectide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the

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passociated with an aberrant inflammatory, response such as asthma, bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Retter's syndrome, psoriasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polymucleotide sequence represents DNA relating to the human 5-
      diagnosing and/or prognosing disorders
                                                                                                                                                                                                                                                              lipoxygenase (5-LO) gene of the invention
   invention are useful
8$33333333333
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Sequence 168174 BP; 46808 A; 36442 C; 36942 G; 46474 T; 0 U; 1508 Other;

Gaps ö Length 168174; 0; Indels 94.1%; Score 48; DB 6; Le 100.0%; Pred. No. 8.9e-06; iive 0; Mismatches 0; Conservative

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166822 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 166869 51 4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT a à

RESULT 2 ABT11114

ABT11114 standard; DNA; 168273

ABT11114;

(first entry) 05-DEC-2002

Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.

Human; polymorphic region; 5-lipoxygenase; 5-LO gene; asthma; bronchitis; sinusitis; ulcerative colitis; nephritis; amyloidosis; sarcoidosis; rheumatoid arthritis; scleroderma; lupus; non-allergic rhinitis; polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;

Homo sapiens.

WO200262825-A2.

15-AUG-2002.

07-FEB-2002; 2002WO-US003546.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC

Meyer J; D, Ваглев WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma.

Disclosure; Fig 2; 290pp; English.

The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the present invention are useful for diagnosing and/or prognosing disorders associated with an aberrant inflammatory response such as asthma, bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory

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Gaps

.; 0

Indels

9

0; Mismatches

DB 6; Length 13249;

Score 38.4; DB 6; Pred. No. 0.0082;

ch 75.3%; 1 Similarity 87.5%; 42; Conservative

Best Local Similarity

Matches

Query Match

Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system discorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polynuclectide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirhemmatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                       Sequence 168273 BP; 46834 A; 36467 C; 36966 G; 46498 T; 0 U; 1508 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                  166921 AAAAGAAATIGGACTIAAAGITAAATACTITITGIGCTICAAACATCAT 166968
                                                                                                                                                                                ;
0
                                                                                                                                              Length 168273;
                                                                                                                                                                                                                     21
                                                                                                                                                                                                                  AAAAGAAATIGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 89; 32pp + Sequence Listing; German.
                                                                                                                               DB 6; Lens.
1. 8.9e-06;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 89.
                                                                                                                                          94.1%; Score 48; DB 100.0%; Pred. No. 8.9
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                                                                                                                                                                                                                                                                                                                                        ABL32116 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                           ABL32116;
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                                                                                                                                                                              Matches
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite of also disclosed are oligonuclectides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the cytosine methylation state (CpG islands) of these genes, and a method contain eas associated with signal transduction. The genomic DNA can be contained from cells or cellular components which contain DNA, e.g. cell inter, biopsise, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, cand all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK311545 represent committee date for this patent did not form part of the printed sequence date for this patent did not form part of the printed for the form parent of the printed for the form the
                                                                                                                                      Human, signal transduction associated gene, cytosine methylation state, CpG island, signal transduction associated disease, solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                             Signal transduction associated gene modified complementary DNA #10.
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.larity 87.5%; Pred. No. 0.0082;
Conservative 0; Mismatches 6; Indels 0;
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                       (first entry)
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                          23-APR-2002
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                                                                                                                                                                                                                                                                                   Synthetic
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ID ABK3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective; anti-HIV; anticonvulsant, ophthalmological; antirhematic, antiartitic; antidiabectic, antipsoriatic, antiartiac, antiinflammatory; cancer; eye disease, arteriosclerosis, anaemia; acute myeloid leukaemia; Alzheimer's disease, AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system disease; cytosine methylation; antiasthmatic;
                                               Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
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              4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 90; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                         system associated gene SEQ ID NO: 90.
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75.3%; Score 38.4; DB 6;
Best Local Similarity 87.5%; Pred. No. 0.0082;
Matches 42; Conservative 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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01-SEP-2000; 2000DE-01043826
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Gaps

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9541

Signal transduction associated gene modified DNA #10.

ABK31177

ABK31177/c ID ABK3117 XX AC ABK311

RESULT 5

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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite.

Also disclosed are oligomucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the cytosine methylation state (CpG islands) of these genes, and a method of contained from cells or cellular components which contain DNA, e.g. cell chars, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK311545 represent committed for the signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed sequence. The process of the contained from the printed of the printed sequence data for this patent did not form part of the printed sequence.
                 Human, signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38.4; DB 6; Length 13249;
Pred. No. 0.0082;
0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 19; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                                                                                           29-JUN-2001; 2001WO-EP007472.
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01-SEP-2000; 2000DE-01043826.
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ilarity 87.5%;
Conservative (
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les 42; Conserv
                                                                                                                                                          WO200200926-A2.
                                                                                                  sapiens
                                                                                                                                                                                                     03-JAN-2002
                                                                                                                     Synthetic
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                                                                                                  Homo
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The invention relates to a nucleic acid comprising a sequence of at least lab bases of a segment of chemically pretreated DNA of genes associated with cell signaling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as an each of PNA-oligomers for signalling, as well as an enthod which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the

Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.

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Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS

WPI; 2002-154758/20.

29-JUN-2001; 2001WO-EP007471 30-JUN-2000; 2000DE-01032529 01-SEP-2000; 2000DE-01043826

WO200202807-A2

10-JAN-2002

Unidentified

Claim 1; SEQ ID NO 22; 24pp + Sequence Listing; English.

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6; Length 13249;

Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;

Query Match

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signalling; cytosine methylation; cell signalling disease; cancer;
                           Gaps
                         0;
                                                                  51
                                             4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGGGGTTCAAACATCAT
                                                                                                                                                                                               Chemically treated cell signalling DNA sequence#11.
ch 75.3%; Score 38.4; DB 6; ]
1 Similarity 87.5%; Pred. No. 0.0082;
42; Conservative 0; Mismatches 6;
                                                                                                                           ABL70131 standard; DNA; 13249
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                                                                                                                                                                       01-JUL-2002 (first entry)
                                                                                                                                                                                                                                tumour; cytostatic; ds
            Local Similarity
                                                                                                                                                                                                                                                                             WO200202807-A2
                                                                                                                                                                                                                                                       Unidentified,
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Matches
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Gaps

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ABL70132 standard; DNA; 13249 BP

4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT

Cell signalling; cytosine methylation; cell signalling disease; cancer; tumour; cytostatic; ds.

Chemically treated cell signalling DNA sequence complementary to#11.

(first entry)

01-JUL-2002

ABL70132/c
ID ABL70132/c
XX AC ABL7013
XX DT 01-JULDY Chemics
XX Cell si
KW Cell si
XX tumour;

ABL70132;

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signaling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is signalling, as well as a cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell categories well as a method which is categories for particularly suitable for the diagnosis and/or therapy of genetic and parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABLYONIL-ABLYONGSE represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed provided by the invention supplied by the
                                                                                                                                                                              Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 21; 24pp + Sequence Listing; English
                                                                                            Berlin K;
  01-SEP-2000; 2000DE-01043826.
                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buropean Patent Office
                                           (EPIG-) EPIGENOMICS AG
                                                                                            olek A,
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Gaps Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other; ; 0 6; Length 13249; Score 38.4; DB 6; Lengtn L. Pred. No. 0.0082; 6; Indels 0; Mismatches 75.3%; Local Similarity 87.5 tes 42; Conservative Query Match Matches

o;

21 4 AAAAGAAATIGGACTIAAAGTIAAAIACTITIGIGCTICAAACAICAI ਨੋ g

ACA39547 standard; DNA; 879 19-JUN-2003 (first entry) ACA39547;

Prokaryotic essential gene #21204.

Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

Mycoplasma genitalium.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851.

(ELIT-) ELITRA PHARM INC.

06-MAR-2002; 2002US-0362699P

Zyskind JW; Xu HH; Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

2003-029926/02

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 27417; 1766pp; English.

the inventory fraction of a coll data of the collection where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid;

(2) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular croproliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits callular proliferation or the biological dentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent of to which each of the strains is present in a culture or collection of strains; or (13) identifying proteins or serial act monotogous nucleic acids required the collection of an organism. The antisense nucleic acids required collection of druc discovery propressed or the candidate molecic acids required for collection of the cellular proprises of the centing for homologous nucleic acids required for cellular proprises. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumonnae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences The invention relates to an isolated nucleic acid comprising any

Sequence 879 BP; 269 A; 120 C; 143 G; 347 T; 0 U; 0 Other;

Gaps ; 0 DB 7; Length 879; 14; Indels 56.1%; Score 28.6; DE 72.5%; Pred. No. 8.8; ive 0; Mismatches 37; Conservative Best Local Similarity Query Match Matches

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537 ACTAAAAGGATTTGGAATGAAGTAGAATACTTTTTTCCTTTAACAGTAAT 487 1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51 ò g

ACC69139 standard; DNA; 10809 ACC69139; RESULT 10 ACC69139/

(first entry) 10-JUL-2003

M. genitalium aerobic metabolism gene cassette DNA SEQ ID NO:7.

Mycoplasma genitalium; gene cassette; replication; transcription; translation; metabolism; basic genetic operating system; gene therapy; autonomous protetrophic nanomachine; nanomachine; nanomachine; bioreactor; bioremediation; therapeutic; delivery system; artificial tissue; artificial organ system; energy conversion system; processing system; anabolic system; catabolic system; biological film; biological coating; cosmetic; gene; ds.

Mycoplasma genitalium.

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2001-514838/56.
                                                                                                                                                                                                         Similarity
37; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAO03215.
                                                                      Fragment Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                              AAT58840_3
AAT58840_4
                                                        Sequence split
                                                                                                    AAT58840_1
AAT58840_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001.
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                                                                                                                                                          AAT58840
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                                                                                                                                                                                                                                                                                                                                                                                          AAI83146;
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                             Local
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                            AAT58840
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Continuation (6 of 6) of AAT58840 from base 500001 (Mycoplasma genitalium genome.)
WP Sequence split into 6 fragments LOCUS AAT58840 Accession Aat58840
WP AAT58840 1 10000
WP AAT58840 2 200001 310000
WP AAT58840 3 300001 410000
WP AAT58840 400001 510000
WP AAT58840 5 500001 50000
                                                                                                                                                                                                                                                                                                          The present invention describes a basic genetic operating system for an autonomous prototrophic or auxotrophic nanomachine comprising a nanomachine genome encoding a minimal gene set sufficient for viability or replication, optionally in the presence of an auxotrophic molecule.

Also described is an autonomus prototrophic or auxotrophic nanomachine comprising a basic genetic operating system for autorrophic nanomachine or auxotrophic molecule, and a particle envelope. The nanomachines can be used in gene therapy. The basic genetic operating system or nanomachine or used in gene therapy. The basic genetic operating system or nanomachine or used in therapeutic, diagnostic and industrial applications, e.g. as a bioreactor, for bioremediation, for the production of a therapeutic biomolecule or as a therapeutic reagent, for the production of a therapeutic calagnostic indicator or reagent, as a delivery system, as an artificial tissue or organ system, as an energy conversion system, as a processing system, as an anabolic or catabolic system, for the production of system, as an anabolic or catabolic system, for the production of sequence represents a Mycoplasma genitalium gene cassette nucleotide sequence, which is used in an example from the present invention for the design and synthesis of a basic genetic operation system for a
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                                                                                                                                                                                                           New basic genetic operating system for autonomous prototrophic or autocrophic nanomachine, useful for therapeutic, diagnostic or industrial purposes, comprises a nanomachine genome encoding a gene set for viability or replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4241 ACTAAAAGGATÍTIGGAATGAAGTAGAATACTÍTÍTITICCTÍTTAACAGTAAT 4191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10809 BP; 3805 A; 1468 C; 1932 G; 3604 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACAAAAAGAAATIGGACTIAAAGTIAAATACTITIGIGCTICAAACATCAT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
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Best Local Similarity 72.5%; Pred. No. 10;
Matches 37; Conservative 0; Mismatches 14; Indels
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Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                     Example 1; Page 210-213; 250pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replication competent nanomachine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.1%;
                                                           18-SEP-2002; 2002WO-US029811
                                                                                        20-SEP-2001; 2001US-00960870
                                                                                                                      (EGEA-) EGEA BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37; Conservative
                                                                                                                                                                               WPI; 2003-354602/33
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WO2003025145-A2
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Best Local (
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Continuation (5 of 6) of AATS8840 from base 400001 (Mycoplasma genitalium genome. )
WP Sequence split into 6 fragments LOCUS AATS8840 Accession Aat58840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ů
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunochlatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
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                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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Pred. No. 12;
0; Mismatches
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310000
410000
510000
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18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI83146 standard; cDNA; 355
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72.5%;
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400001
500001
                                                                                                                                             100001
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(first entry)

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Apoptosis; HIV; Bloom syndrome; cardiopathy; neurodegenerative disorder; Herpes simplex virus; renal ischaemia; amyotrophic lateral sclerosis;
                                                                                                                                                                                                 Chemically treated apoptosis gene complementary to gene #31.
                                                 ABL54362 standard; DNA; 5864 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-UUN-2000; 2000DE-01035252.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                 WO200177164-A2
                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                   29-JUL-2002
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                                                                                                                                                                                                                                                                                                 cancer; ds
                                                                                                  ABL54362;
RESULT 15
ABL54362/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; antiantective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antispsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful f
diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                  Gaps
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                                                 Length 355;
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                                                                                               11; Indels
                                                                                                                                                GTGCTTCAAACATCA 50
Sequence 355 BP; 86 A; 65 C; 74 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 1414.
                                                 DB 4;
                                              Score 26.4; DB
Pred. No. 41;
0; Mismatches
                                                                                                                                              7 AGAAATTGGACTTAAAGTTAAATACTTT
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                                              Query Match 51.8%;
Best Local Similarity 75.0%;
Matches 33; Conservative
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Best Local Similarity 70.8%;
Matches 34; Conservative
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ABL33441/C
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                                                                                                                                                                             Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer.
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70.8%; Pred. No. 89;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                      Claim 1; Seq ID #62; 24pp; English.
                                                               Berlin K;
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                                                               Piepenbrock C,
(EPIG-) EPIGENOMICS AG
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                                                                                                                           WPI; 2002-017444/02
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Best Local Similarity
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Gaps

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1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACAT 48

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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May 7, 2004, 13:24:59 ; Search time 531.669 Seconds (without alignments) 4157.648 Million cell updates/sec acaaaaagaaattggactta......ttttgtgcttcaaacatcat 51 US-10-071-411A-1_COPY_450_500 OM nucleic - nucleic search, using sw model Title: Perfect score: Sequence: Run on:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6940541 Total number of hits satisfying chosen parameters:

3470272 seqs, 21671516995 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries GenEmbl:* Database :

9b ba: *
9b htg: *
9b om: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score or the result being printed,		
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RESULT 1	AL731567	LOCUS	DEFINITION		ĕ	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

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During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone mane. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
one plasmid subclone or more than one Mil subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr:, TREMBL; Wp:, WORNDEP; Information on the WORNDEP
thtp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
RAPI:67C2 is from the library RPOI-11:1 constructed by the group of
pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PRACES:
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1-16P14, WORKING DRAFT SEQUENCE, 30 unordered
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-16P14
          Trust Sanger Institute, Hinxton,
Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CBIO 18A, UK. B-mail enquiries in the cast of the cast of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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'db_xref="taxon:9606"
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Homo sapiens (human)
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Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Norman, C. H., O'Connor, T., O'Domell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Phirect Submission
                                                                                                                                                                                                                                                                                             Submitted Mission 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 14, 2000 this sequence version replaced gi:6524208.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washing.on.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 16 P 14
Sequencing vector: M13, M78815, 100% of reads
Sequencing vector: M13, M78815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 111055 bases at least Q40
Consensus quality: 115056 bases at least Q30
Consensus quality: 11505 bases at least Q20
Insert size: 1570500; agarose-fp
Insert size: 157754; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L3606
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of 668 bp in length
100 bp
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AC010862 194453 bp DNA linear HTG 30-AUG-2001
Homo sapiens chromosome 06 clone RPI1-326D18, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
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Direct Submission
Direct Submission
Submitted (25-SEP-1999) Genome Therapeutics Corporation, 100 Beaver
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (base) to 194453)
Smith, D.R.
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On Sep 1, 2000 this sequence version replaced gi:8247773.
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Web site: http://www.genomecorp.com/
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AC010862.7 GI:9957987
HTG: HTGS FHASE1; HTGS_DRAFT; HTGS_CANCELLED.
Homo sapiens (human)
Homo sapiens (contacts) Craniata; Verte
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145798. .160654-
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120220: contig of 11717 bp in length
120320: gap of 100 bp
132058: contig of 12638 bp in length
133058: gap of 100 bp
145697: contig of 12639 bp in length
145797: gap of 100 bp
160654: contig of 14857 bp in length
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252. .1760
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 20 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Pred. No. 0.33;
0; Mismatches 6;
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/mol type="unassigned DNA"
/db xref="taxon:32630"
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Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek, A., Piepenbrock, C. and Berlin, K.
                               94.1%; Score 48; DB 100.0%; Pred. No. 0.0 iive 0; Mismatches
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Sequence 19 from Patent W00200926.
AX344172
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Sequence 20 from Patent WO0200926.
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1 Similarity 87.5%;
42; Conservative 0
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Best Local Similarity 87.5%;
Matches 42; Conservative
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AX344173/c
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Assembly program: Phrap, version 990315
Consensus quality: 162991 bases at least Q40
Consensus quality: 176452 bases at least Q30
Consensus quality: 179870 bases at least Q20
Insert size: 192053; sum-of-contigs
Quality coverage: 4.2x in Q20 bases; sum-of-contigs
                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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75325: gap of unknown length
85420: contig of 10095 bp in length
85205: gap of unknown length
101985: contig of 16365 bp in length
101985: gap of unknown length
124008: contig of 22023 bp in length
124108: gap of unknown length
157199: contig of 33091 bp in length
157299: gap of unknown length
157299: gap of unknown length
157299: gap of unknown length
194453: contig of 37154 bp in length
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37061: gap of unknown length
43997: contig of 6936 bp in length
44097: gap of unknown length
49940: contig of 5843 bp in length
50040: gap of unknown length
56987: contig of 6947 bp in length
57087: gap of unknown length
55541: contig of 8454 bp in length
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gap of unknown
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    194453
/organism="Homo sapiens"

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/chromosome="06"
/clone="RP11-326D18"
/clone_lib="RPCI-11"
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synthetic construct
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                                                                                                                                                                                                                                     /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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/mol_type="unassigned DNA"
/db_xref="taxon.32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                                                     Olek, A., Piepenbrock, C. and Berlin, K.
Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 89 03-JAN-2002;
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Diagnosis of diseases associated with the immune system
Patent: WO 0200328-A 90 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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                                      linear
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Pred. No. 0.33;
0; Mismatches
                                                                                                                                                                                                                                                                                                                        75.3%; Score 38.4; DB 87.5%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                   AX345018 13249 bp
Sequence 89 from Patent W00200928.
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Seguence 21 from Patent W00202807.
AX348563
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Sequence 90 from Patent WO0200928.
AX345019
                                                                                                                                                                                               Epigenomics AG (DE)
Location/Qualifiers
1. 13249
                                                                           AX345018.1 GI:18492904
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1 Similarity 87.5%;
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        RESULT 6
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ALS90439 192044 bp DNA linear PRI 23-AUG-2001
Complete sequence.
ALS90439.12 GI:15384822
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 192044)

                                                                                                             1. 13249-
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Direct Submission
Submitted (23-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Olek, A., Piepenbrock, C. and Berlin, K.
Diagnosis of diseases associated with cell signalling
Patent: WO 0202807-A 21 10-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Diagnosis of diseases associated with cell signalling
Patent: WO 0202007-A 22 10-JAN-2002;
Epigenomics AG (DB)
Location/Qualifiers
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75.3%; Score 38.4; DB
Best Local Similarity 87.5%; Pred. No. 0.33;
Matches 42; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX348564
Sequence 22 from Patent WO0202807.
AX348564
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COMMENT

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Summary Statistics of Consensus quality: 124565 bases at least Q30 Consensus quality: 124565 bases at least Q30 Serimated insert size: 127829; sum-of-contigs estimation Quality coverage: 4.18 in Q20 bases; pulse field gel estimation Quality coverage: 4.18 in Q20 bases; pulse field gel estimation. The size at working draft's sequence. It currently consists of 16 contigs. Gaps between the contigs. This is a working draft's sequence it currently are represented as runs of N. The order of the pieces of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the submittor.**

**This sequence will be preserved.**

**Pins against sequence as soon as it is available and the accession number will be preserved.

**Pins against sequence will be preserved.**

**Pins against sequence will sequence wil
   Gaps
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Pred. No. 3.8;
0; Mismatches 9; Indels 0;
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/clone="CTD-2235Al3"
/clone_lib="CalTech human BAC library D"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                Center clone name: CITB-H1_2235A13
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/organism="Homo sapiens'
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/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                      Center Project Name: 717802
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81.2%;
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                                                                                                                                                                                                                                                     Project Information
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Best Local Similarity 81.2:
Matches 39; Conservative
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83264
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      JOURNAL
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                                                                 COMMENT
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         Triquevies: Cloud this sequence version replaced gi:14268248.

On Aug 31, 2001 this sequence version replaced gi:14268248.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSEROT; Ir:, TREMBL; WP., WORMPEP; information on the WORMPEP when, we have and a the found a the formation on the MORMPEP when, we have a series of the following series on be found a at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPII-394123 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RPII-394123 is at 192044 in this sequence. The true left end of clone RPII-657A9 is at 85254 in this sequence. The true right end of clone RPII-3945 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128529 bp DNA linear HTG 18-JUL-2000 Homos aapiens chromosome 5 clone CTD-2235A13, WORKING DRAFT SEQUENCE, 16 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at Mapping Group. Further information can be found at RRPI-394123 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
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0; Mismatches
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
/mol type="genomic DNA"
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/clone lib="RPCI-11.2"
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Sequencing of Human Chromosome
Unpublished
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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DOE Joint Genome Institute.
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FEATURES

AC025758/c DEFINITION

ACCESSION

KEYWORDS

REFERENCE AUTHORS

REFERENCE AUTHORS TITLE

JOURNAL

TITLE

Matches

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DEFINITION

RESULT 12

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AC008810

ACCESSION VERSION KEYWORDS

ORGANISM

AUTHORS
TITLE
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REFERENCE AUTHORS TITLE

JOURNAL REFERENCE

TITLE JOURNAL AUTHORS

COMMENT

FEATURES

ORIGIN

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BS000239 209016 bp DNA linear PRI 07-OCT-2003 Pan troglodytes chromosome 22 clone:PTB-153E07, map 22, complete sequences.
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*Chinase National Human Genome Center at Shanghai, Shanghai, China;
*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
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2 (bases 1 to 209016)

1sai, S., Liu, T., Wu, K., Liao, T. and Hsiao, K.

1sai, S., Liu, T., Wu, K., Liao, T. and Hsiao, K.

Submitted (16-MAY-2003) Shih-Feng Tsai, National Health Research
Institutes (MHRI), Division of Molecular and Genomic Medicine; 128,
Yen-Chiu-Yuan Road, Sec 2, Taipei 115, Taiwan

Tel:866-2-28267319, Fax:886-2-28200552) www.nhri.org.tw/,
                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, DOB Joint
Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 164217)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (01-FEB-2002) DOB Joint Genome Institute, 2800 Mitchell
Dirive, Walnut Creek, CA 94598, USA
On Feb 1, 2002 this sequence version replaced gi:15193398.
Draft Sequence Produced by DOE Joint Genome Institute
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (abses 1 to 16421?) DOB Joint Genome Institute and Stanford Human Genome Center.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.dom
Ouality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-263G2"
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2 (bases 1 to 164217)
DOB Joint Genome Institute.
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Homo sapiens (human)
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Best Local Similarity
Matches 39; Conserva
                           Homo sapiens
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Dobe Joint Genome Institute.

Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission

Direct Submission

Dived (28-0704-2003) DOB Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94599, USA

On Jun 28, 2003 this sequence version replaced gi:14993661.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (26-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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Darbour Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

Submitted Comme Institute and Stanford Human Genome Center.
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DOB Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                          ACO08810 157325 bp DNA linear PRI 28-JUN
Homo sapiens chromosome 5 clone CTD-2096123, complete sequence
ACO08810
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                         3 AAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA 50
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Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.3.
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/db_xref="taxon:9606"
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/clone="CTD-2096123"
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Matches 39; Conserval
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ACCESSION
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RESULT 13 AC093264 LOCUS

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KEYWORDS

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Gaps

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Direct Submission

Submitted (19-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Apr 7, 2002 this sequence version replaced gi:14141369.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em; EMBL; Sw;

SMISSROT; Tr:, TREMBL; Wp:, WORWBEP; Information on the WORWBEP

database can be found at.
                                                                                                                                                                                                                                                                                                                                                                                                                   ROD 29-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                               AL365334 173053 bp DNA linear ROD 29-JUN-2002
Mouse DNA sequence from clone RP23-392F1 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
1 (bases 1 to 173053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-392F1 is from the RPC1-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                         123272 AAATAAATAAATTGGGCTTAAAATTAAAACTTTGGGCTTGCAAGGACAT 123222
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                                                                                         Length 209016;
                                                                                                                                                                                                           1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                Indels
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                                                                                      ch 65.5%; Score 33.4; DB 9; Similarity 78.4%; Pred. No. 3.8; 40; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: UK Medical Research Council
Center code: UK-MRC
Web site: http://mrcseg.har.mrc.ac.uk
'note="low quality region"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="1"
/clone="RP23-392F1"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.6
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Best Local Similarity
Matches 38; Conserv
                                                                                                                    Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                        RESULT 15
AL365334/c
                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Source information:
The PTB1 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This entry has been annotated with sequence estimates computed by the Phrap assembly program. All manually edited base been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in
                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly
program: Phragpy version 0.993319
Consensus quality: 207,750 bases at least Q40
Consensus quality: 207,996 bases at least Q30
Consensus quality: 208,014 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="gap containing unresolved di-nucleotide repeats,
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany, *National Institute of Genetics, Mishima, Japan; *National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an attempt was made to resolve all sequencing problems, such compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neighboring clones: PTB-152N20(left) and RP43-055A16(right) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones may be obtained from Asao Fujiyama and co-workers (http://www.gsc.riken.go.jp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                    *RIKEN Genomic Sciences Center, Yokohama, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="PTB-153E07"
/clone lib="PTB1 chimpanzee BAC"
16459. ..16463
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46232. .46235
/note="low quality region"
46277. .46280
/note="low quality region"
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/mol type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="22"
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128691
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/note="low quality region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Quality Assessment:
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                                                                                                                                                                                                                                                                                                                                                        clone name: HI
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Search completed: May 7, 2004, 14:30:58 Job time : 538.003 sec8